

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 15:41:08 ; Search time 33.4091 Seconds

(without alignments)
277.441 Million cell updates/sec

Title: US-09-744-875A-1

Perfect score: 21

Sequence: 1 agattctcagaatccaatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 segs, 220691566 residues

830498

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	18	85.7	21	1	US-08-366-276-8	Sequence 8, Appli
2	18	85.7	100	4	US-09-522-217-59	Sequence 59, Appli
3	18	85.7	100	4	US-09-522-217-60	Sequence 60, Appli
4	15.4	73.3	24	4	US-08-369-754-1	Sequence 1, Appli
5	14.6	69.5	58	3	US-09-140-804-46	Sequence 46, Appli
6	14.6	69.5	58	4	US-09-173-043-22	Sequence 22, Appli
7	14.6	69.5	58	4	US-09-209-525-42	Sequence 42, Appli
8	14.6	69.5	58	4	US-09-686-838B-46	Sequence 46, Appli
9	14.2	67.6	20	4	US-09-662-402A-35	Sequence 35, Appli
10	13.8	65.7	30	1	US-08-201-697-12	Sequence 12, Appli
11	13.8	65.7	30	1	US-08-463-090B-24	Sequence 24, Appli
12	13.6	64.8	34	1	US-08-332-420-54	Sequence 54, Appli
13	13.6	64.8	37	1	US-07-941-363-1	Sequence 1, Appli
14	13.6	64.8	38	3	US-09-143-634-28	Sequence 28, Appli
15	13.6	64.8	40	1	US-08-308-196A-4	Sequence 4, Appli
16	13.6	64.8	40	3	US-09-289-803-3	Sequence 3, Appli
17	13.6	64.8	40	5	PCT-US91-06452-4	Sequence 4, Appli
18	13.6	64.8	41	3	US-09-289-803-2	Sequence 2, Appli
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21	13.4	63.8	30	3	US-09-030-613-30	Sequence 30, Appli
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27	13.2	62.9	25	4	US-09-402-776-5	Sequence 5, Appli

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C 29	13.2	62.9	25	5	PCT-US93-08849-5	Sequence 5, Appli
C 30	13.2	62.9	31	3	US-09-182-816-30	Sequence 30, Appli
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C 37	13.2	62.9	33	4	US-08-169-715-47	Sequence 47, Appli
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110	12.2	58.1	24	1	US-08-125-012-28	Sequence 28, Appli	183	12	57.1	30	4	US-09-696-322-6	Sequence 6, Appli
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173	12.2	57.1	30	4	US-09-590-776-6	Sequence 6, Appli	246	11.8	56.2	30	4	US-09-170-496D-102	

C 247	11.8	56.2	30	PCT-US95-05980-70	Sequence 70, Appl	320	11.6	55.2	64	4	US-10-013-784-9	Sequence 9, Appl
C 248	11.8	56.2	32	US-08-305-764C-7	Sequence 7, Appl	321	11.6	55.2	65	3	US-09-415-522-28	Sequence 28, Appl
249	11.8	56.2	33	US-08-456-840-41	Sequence 41, Appl	322	11.6	55.2	66	3	US-08-392-455-45	Sequence 45, Appl
250	11.8	56.2	33	US-08-266-407A-41	Sequence 41, Appl	323	11.6	55.2	66	5	PCT-US91-08525-45	Sequence 45, Appl
251	11.8	56.2	33	US-08-892-544-41	Sequence 41, Appl	324	11.6	55.2	69	1	US-08-220-151-27	Sequence 27, Appl
C 252	11.8	56.2	33	US-09-298-745-2	Sequence 2, Appl	325	11.6	55.2	69	1	US-08-413-118-27	Sequence 27, Appl
C 253	11.8	56.2	33	US-09-474-178-6	Sequence 6, Appl	326	11.6	55.2	69	1	US-08-224-657-4	Sequence 4, Appl
C 254	11.8	56.2	35	US-09-528-271-17	Sequence 17, Appl	327	11.6	55.2	69	1	US-08-257-073-72	Sequence 72, Appl
255	11.8	56.2	41	US-08-860-882A-34	Sequence 34, Appl	328	11.6	55.2	69	2	US-08-184-009-4	Sequence 4, Appl
256	11.8	56.2	41	US-08-860-882A-66	Sequence 66, Appl	329	11.6	55.2	69	2	US-08-486-969-4	Sequence 4, Appl
257	11.8	56.2	41	US-09-011-769A-1	Sequence 1, Appl	330	11.6	55.2	69	2	US-08-417-210A-4	Sequence 4, Appl
C 258	11.8	56.2	41	US-09-011-769A-49	Sequence 49, Appl	331	11.6	55.2	69	2	US-08-458-356-4	Sequence 4, Appl
C 259	11.8	56.2	45	US-08-997-918-2	Sequence 2, Appl	332	11.6	55.2	69	2	US-08-471-022-4	Sequence 4, Appl
260	11.8	56.2	45	US-08-997-918-33	Sequence 33, Appl	333	11.6	55.2	69	3	US-08-473-446-27	Sequence 27, Appl
261	11.8	56.2	47	US-09-641-638-829	Sequence 829, App	334	11.6	55.2	69	3	US-08-460-736-4	Sequence 4, Appl
C 262	11.8	56.2	47	US-09-851-120-2	Sequence 2, Appl	335	11.6	55.2	69	4	US-09-354-138-4	Sequence 4, Appl
C 263	11.8	56.2	47	US-09-422-978-1257	Sequence 1257, Ap	336	11.6	55.2	69	4	US-09-535-370-4	Sequence 4, Appl
C 264	11.8	56.2	48	US-08-477-254A-31	Sequence 31, Appl	337	11.6	55.2	69	5	PCT-US96-00547-4	Sequence 4, Appl
C 265	11.8	56.2	48	US-08-472-576B-31	Sequence 31, Appl	338	11.6	55.2	72	1	US-08-477-877B-70	Sequence 70, Appl
C 266	11.8	56.2	48	US-08-428-734B-31	Sequence 31, Appl	339	11.6	55.2	72	1	US-08-472-281A-70	Sequence 70, Appl
C 267	11.8	56.2	48	US-08-713-556F-31	Sequence 31, Appl	340	11.6	55.2	72	2	US-08-301-593-72	Sequence 72, Appl
C 268	11.8	56.2	50	US-09-528-271-1	Sequence 1, Appl	341	11.6	55.2	72	4	US-09-301-593-72	Sequence 72, Appl
C 269	11.8	56.2	50	US-09-528-271-2	Sequence 2, Appl	342	11.6	55.2	72	4	US-09-301-593-77	Sequence 77, Appl
C 270	11.8	56.2	50	US-09-528-115-4	Sequence 4, Appl	343	11.6	55.2	75	4	US-08-973-398-9	Sequence 9, Appl
C 271	11.8	56.2	50	US-09-528-115-5	Sequence 5, Appl	344	11.6	55.2	87	2	US-08-631-751A-4	Sequence 4, Appl
C 272	11.8	56.2	51	5318899-30	Patent No. 5318899	345	11.6	55.2	97	5	PCT-US94-06456-12	Sequence 12, Appl
C 273	11.8	56.2	64	US-08-153-071-4	Sequence 4, Appl	346	11.6	55.2	97	5	PCT-US94-06456-41	Sequence 41, Appl
C 274	11.8	56.2	64	US-08-609-271-11	Sequence 11, Appl	347	11.6	55.2	98	5	US-08-210-222-22	Sequence 22, Appl
C 275	11.8	56.2	64	US-08-438-511-4	Sequence 4, Appl	348	11.6	55.2	98	5	PCT-US94-06456-20	Sequence 20, Appl
C 276	11.8	56.2	64	US-08-487-431-7	Sequence 7, Appl	349	11.6	55.2	98	5	PCT-US94-06456-49	Sequence 49, Appl
C 277	11.8	56.2	64	US-08-188-374-11	Sequence 11, Appl	350	11.4	54.3	15	2	US-08-585-684B-2073	Sequence 2073, Ap
C 278	11.8	56.2	64	US-08-973-629-7	Sequence 7, Appl	351	11.4	54.3	15	3	US-09-038-073-2073	Sequence 2073, Ap
279	11.8	56.2	65	US-09-482-180A-17	Sequence 17, Appl	352	11.4	54.3	17	5	US-08-308-196A-5	Sequence 5, Appl
C 280	11.8	56.2	76	5314995-6	Patent No. 5314995	353	11.4	54.3	17	5	PCT-US91-06452-5	Sequence 5, Appl
C 281	11.8	56.2	100	US-09-565-241-19	Sequence 19, Appl	354	11.4	54.3	18	2	US-08-174-672D-57	Sequence 57, Appl
C 282	11.6	55.2	25	US-08-477-877B-15	Sequence 15, Appl	355	11.4	54.3	20	2	US-08-616-844-42	Sequence 42, Appl
C 283	11.6	55.2	25	US-08-472-281A-15	Sequence 15, Appl	356	11.4	54.3	20	2	US-08-599-654-42	Sequence 42, Appl
C 284	11.6	55.2	25	US-08-477-989B-15	Sequence 15, Appl	357	11.4	54.3	20	3	US-08-944-868A-42	Sequence 42, Appl
C 285	11.6	55.2	26	US-08-477-877B-82	Sequence 82, Appl	358	11.4	54.3	20	3	US-08-944-423A-42	Sequence 42, Appl
C 286	11.6	55.2	26	US-08-472-281A-82	Sequence 82, Appl	359	11.4	54.3	20	3	US-08-944-446-42	Sequence 42, Appl
C 287	11.6	55.2	26	US-08-349-696-10	Sequence 10, Appl	360	11.4	54.3	20	3	US-09-313-932-352	Sequence 352, App
C 288	11.6	55.2	30	US-08-233-009-10	Sequence 10, Appl	361	11.4	54.3	20	3	US-09-313-932-356	Sequence 356, App
C 289	11.6	55.2	30	US-08-560-231-10	Sequence 10, Appl	362	11.4	54.3	20	3	US-09-198-442A-6760	Sequence 6760, Ap
C 290	11.6	55.2	30	US-08-174-672D-11	Sequence 11, Appl	363	11.4	54.3	22	3	US-09-297-535-5	Sequence 5, Appl
291	11.6	55.2	30	US-08-080-704A-10	Sequence 10, Appl	364	11.4	54.3	22	3	US-09-297-535-6	Sequence 6, Appl
C 292	11.6	55.2	30	US-09-243-560B-8	Sequence 8, Appl	365	11.4	54.3	25	1	US-08-073-807A-14	Sequence 14, Appl
C 293	11.6	55.2	30	US-08-390-850-219	Sequence 219, App	366	11.4	54.3	25	2	US-08-672-814D-6	Sequence 6, Appl
295	11.6	55.2	31	US-08-390-850-220	Sequence 220, App	367	11.4	54.3	25	3	US-09-333-696-6	Sequence 6, Appl
296	11.6	55.2	31	US-08-390-850-221	Sequence 221, App	368	11.4	54.3	25	4	US-09-282-218A-6	Sequence 259, App
297	11.6	55.2	31	US-08-390-850-330	Sequence 330, App	369	11.4	54.3	27	1	US-07-977-284A-259	Sequence 259, App
298	11.6	55.2	31	US-08-390-850-331	Sequence 331, App	370	11.4	54.3	27	1	US-08-599-252-48	Sequence 48, Appl
299	11.6	55.2	31	US-08-390-850-332	Sequence 332, App	371	11.4	54.3	27	1	US-08-647-928-2	Sequence 2, Appl
300	11.6	55.2	31	US-08-390-850-333	Sequence 333, App	372	11.4	54.3	27	2	US-08-256-446B-259	Sequence 259, App
301	11.6	55.2	31	US-08-435-634-219	Sequence 219, App	373	11.4	54.3	27	3	PCT-US96-06352-48	Sequence 48, Appl
302	11.6	55.2	31	US-08-435-634-220	Sequence 220, App	374	11.4	54.3	27	5	PCT-US96-06352-48	Sequence 48, Appl
303	11.6	55.2	31	US-08-435-634-221	Sequence 221, App	375	11.4	54.3	29	5	US-08-408-774A-5	Sequence 5, Appl
304	11.6	55.2	31	US-08-435-634-330	Sequence 330, App	376	11.4	54.3	29	5	PCT-US96-03792-5	Sequence 5, Appl
305	11.6	55.2	31	US-08-435-634-331	Sequence 331, App	377	11.4	54.3	30	2	US-08-888-366-39	Sequence 39, Appl
306	11.6	55.2	31	US-08-435-634-332	Sequence 332, App	378	11.4	54.3	30	3	US-08-888-128-46	Sequence 46, Appl
307	11.6	55.2	31	US-08-435-634-333	Sequence 333, App	379	11.4	54.3	30	3	US-09-115-468-1	Sequence 1, Appl
C 308	11.6	55.2	32	US-08-712-241-20	Sequence 20, Appl	380	11.4	54.3	31	3	US-09-524-845-1	Sequence 1, Appl
C 309	11.6	55.2	32	US-09-242-131A-6	Sequence 6, Appl	381	11.4	54.3	31	4	US-09-525-174-1	Sequence 1, Appl
C 310	11.6	55.2	32	US-09-615-283-6	Sequence 6, Appl	382	11.4	54.3	31	4	US-09-525-258-1	Sequence 1, Appl
C 311	11.6	55.2	33	US-08-192-300-22	Sequence 22, Appl	383	11.4	54.3	31	4	US-09-525-258-1	Sequence 1, Appl
C 312	11.6	55.2	47	US-09-422-978-690	Sequence 690, App	384	11.4	54.3	31	4	US-09-525-258-1	Sequence 1, Appl
C 313	11.6	55.2	47	US-09-422-978-1489	Sequence 1489, Ap	385	11.4	54.3	33	2	US-08-597-541-142	Sequence 142, App
C 314	11.6	55.2	47	US-09-422-978-1713	Sequence 1713, Ap	386	11.4	54.3	33	3	US-09-124-628-142	Sequence 142, App
C 315	11.6	55.2	47	US-09-422-978-3112	Sequence 3112, Ap	387	11.4	54.3	33	3	US-09-127-460-142	Sequence 142, App
C 316	11.6	55.2	49	US-09-647-344A-5	Sequence 5, Appl	388	11.4	54.3	33	3	US-08-496-841C-142	Sequence 142, App
C 317	11.6	55.2	53	US-08-388-029A-49	Sequence 49, Appl	389	11.4	54.3	33	4	US-09-124-523-142	Sequence 142, App
C 318	11.6	55.2	60	5457089-1	Patent No. 5457089	390	11.4	54.3	33	4	US-09-636-756A-142	Sequence 142, App
319	11.6	55.2	64	US-09-653-403-9	Sequence 9, Appl	392	11.4	54.3	34	2	US-08-860-882A-16	Sequence 16, Appl

C 393	11.4	54.3	34	2	US-08-576-626A-22	Sequence 22, Appl	C 466	11.4	54.3	100	3	US-08-483-577A-119	Sequence 119, App
C 394	11.4	54.3	35	3	US-08-235-836C-87	Sequence 87, Appl	C 467	11.4	54.3	100	3	US-08-897-439-119	Sequence 119, App
C 395	11.4	54.3	36	1	US-08-134-570-16	Sequence 16, Appl	C 468	11.4	54.3	100	4	US-08-637-654-119	Sequence 119, App
C 396	11.4	54.3	36	4	US-09-367-750-5	Sequence 5, Appl	C 469	11.4	54.3	100	4	US-08-649-518-119	Sequence 119, App
C 397	11.4	54.3	37	1	US-09-946-678-25	Sequence 25, Appl	C 470	11.2	53.3	20	4	US-09-651-011A-45	Sequence 45, Appl
C 398	11.4	54.3	37	4	US-08-477-877B-27	Sequence 27, Appl	C 471	11.2	53.3	20	4	US-09-198-452A-6470	Sequence 6470, App
C 399	11.4	54.3	37	1	US-08-472-281A-27	Sequence 27, Appl	C 472	11.2	53.3	21	1	US-08-366-276-7	Sequence 7, Appl
C 400	11.4	54.3	37	2	US-08-477-898B-27	Sequence 27, Appl	C 473	11.2	53.3	22	2	US-08-669-753-2	Sequence 2, Appl
C 401	11.4	54.3	38	3	US-08-686-968C-98	Sequence 98, Appl	C 474	11.2	53.3	22	4	US-09-720-201A-9	Sequence 9, Appl
C 402	11.4	54.3	38	3	US-08-235-836C-90	Sequence 90, Appl	C 475	11.2	53.3	23	4	US-09-629-645A-5	Sequence 5, Appl
C 403	11.4	54.3	39	1	US-08-349-867-1	Sequence 1, Appl	C 476	11.2	53.3	23	4	US-09-297-269-2	Sequence 2, Appl
C 404	11.4	54.3	39	1	US-08-239-474A-1	Sequence 1, Appl	C 477	11.2	53.3	24	1	US-08-411-796-194	Sequence 194, App
C 405	11.4	54.3	39	1	US-08-598-305A-1	Sequence 1, Appl	C 478	11.2	53.3	24	1	US-08-411-796-203	Sequence 203, App
C 406	11.4	54.3	39	1	US-08-639-923A-1	Sequence 1, Appl	C 479	11.2	53.3	24	3	US-08-471-039-194	Sequence 194, App
C 407	11.4	54.3	39	2	US-08-732-495-1	Sequence 1, Appl	C 480	11.2	53.3	24	3	US-08-471-039-203	Sequence 203, App
C 408	11.4	54.3	39	2	US-08-686-968C-95	Sequence 95, Appl	C 481	11.2	53.3	24	4	US-08-559-390-194	Sequence 194, App
C 409	11.4	54.3	39	3	US-09-113-750A-20	Sequence 20, Appl	C 482	11.2	53.3	24	4	US-09-331-968A-14	Sequence 14, Appl
C 410	11.4	54.3	39	3	PCT-US95-05431-1	Sequence 1, Appl	C 483	11.2	53.3	24	5	PCT-US93-11198-194	Sequence 194, App
C 411	11.4	54.3	39	5	US-09-626-355-1	Sequence 1, Appl	C 484	11.2	53.3	24	5	PCT-US93-11198-194	Sequence 203, App
C 412	11.4	54.3	41	2	US-08-417-210A-107	Sequence 107, App	C 485	11.2	53.3	25	2	US-08-700-035A-8	Sequence 8, Appl
C 413	11.4	54.3	41	2	US-08-353-400-21	Sequence 21, Appl	C 486	11.2	53.3	25	5	PCT-US96-13457-8	Sequence 8, Appl
C 414	11.4	54.3	44	6	5194376-3	Patent No. 5194376	C 487	11.2	53.3	25	5	US-08-058-299-4	Sequence 4, Appl
C 415	11.4	54.3	45	6	5194376-14	Patent No. 5194376	C 488	11.2	53.3	28	1	US-07-936-163-27	Sequence 27, Appl
C 416	11.4	54.3	45	6	US-09-366-920-7	Sequence 7, Appl	C 489	11.2	53.3	28	1	US-08-482-286A-7	Sequence 7, Appl
C 417	11.4	54.3	47	4	US-09-422-978-1892	Sequence 1892, Ap	C 490	11.2	53.3	28	2	US-08-729-601A-69	Sequence 69, Appl
C 418	11.4	54.3	47	4	US-09-944-243-7	Sequence 7, Appl	C 491	11.2	53.3	28	2	US-08-816-693A-39	Sequence 39, Appl
C 419	11.4	54.3	47	4	US-09-528-271-7	Sequence 7, Appl	C 492	11.2	53.3	29	2	US-08-960-022-26	Sequence 26, Appl
C 420	11.4	54.3	50	4	US-09-528-271-10	Sequence 10, Appl	C 493	11.2	53.3	29	2	US-08-457-254-12	Sequence 12, Appl
C 421	11.4	54.3	51	1	US-08-153-799-1	Sequence 1, Appl	C 494	11.2	53.3	29	3	US-08-885-291-39	Sequence 39, Appl
C 422	11.4	54.3	51	1	US-08-886-967-2	Sequence 2, Appl	C 495	11.2	53.3	29	3	US-09-466-672-39	Sequence 39, Appl
C 423	11.4	54.3	52	3	US-09-306-949-2	Sequence 2, Appl	C 496	11.2	53.3	29	3	US-09-304-232-717	Sequence 717, App
C 424	11.4	54.3	52	3	US-09-307-217-2	Sequence 2, Appl	C 497	11.2	53.3	29	3	PCT-US94-08806-24	Sequence 24, Appl
C 425	11.4	54.3	52	4	US-08-592-029-6	Sequence 6, Appl	C 498	11.2	53.3	29	5	PCT-US95-16626-12	Sequence 12, Appl
C 426	11.4	54.3	54	1	US-08-883-632-6	Sequence 6, Appl	C 499	11.2	53.3	30	1	US-07-998-972A-21	Sequence 21, Appl
C 427	11.4	54.3	54	1	US-08-592-013A-6	Sequence 6, Appl	C 500	11.2	53.3	30	1	US-08-463-953-21	Sequence 21, Appl
C 428	11.4	54.3	54	2	US-08-239-279-18	Sequence 18, Appl	C 501	11.2	53.3	30	1	US-08-462-261-21	Sequence 21, Appl
C 429	11.4	54.3	57	1	US-08-701-269-18	Sequence 18, Appl	C 502	11.2	53.3	30	1	US-08-346-333-3	Sequence 3, Appl
C 430	11.4	54.3	57	1	US-08-417-210A-100	Sequence 100, App	C 503	11.2	53.3	30	1	US-08-346-333-4	Sequence 4, Appl
C 431	11.4	54.3	66	2	US-08-464-073-12	Sequence 12, Appl	C 504	11.2	53.3	30	2	US-08-746-257A-23	Sequence 23, Appl
C 432	11.4	54.3	67	2	US-08-428-252-12	Sequence 12, Appl	C 505	11.2	53.3	30	2	US-09-087-312-2	Sequence 2, Appl
C 433	11.4	54.3	67	2	US-08-416-516A-12	Sequence 12, Appl	C 506	11.2	53.3	30	3	US-09-316-080-6	Sequence 6, Appl
C 434	11.4	54.3	67	3	US-08-402-959A-4	Sequence 4, Appl	C 507	11.2	53.3	30	3	US-09-534-407-7	Sequence 7, Appl
C 435	11.4	54.3	75	4	US-08-238-863-37	Sequence 37, Appl	C 508	11.2	53.3	30	4	US-09-434-690-3	Sequence 3, Appl
C 436	11.4	54.3	81	1	US-08-443-407-37	Sequence 37, Appl	C 509	11.2	53.3	30	4	US-09-511-964-3	Sequence 3, Appl
C 437	11.4	54.3	81	1	PCT-US95-05600-181	Sequence 181, App	C 510	11.2	53.3	30	4	US-09-437-687A-3	Sequence 3, Appl
C 438	11.4	54.3	81	5	US-09-106-182-16	Sequence 16, App	C 511	11.2	53.3	30	4	US-09-007-288F-98	Sequence 98, Appl
C 439	11.4	54.3	86	4	US-09-227-357-3	Sequence 3, Appl	C 512	11.2	53.3	30	4	US-09-999-201B-7	Sequence 7, Appl
C 440	11.4	54.3	86	4	US-09-280-839-6	Sequence 6, Appl	C 513	11.2	53.3	30	5	PCT-US91-07506-4	Sequence 4, Appl
C 441	11.4	54.3	86	4	US-09-411-977-18	Sequence 18, Appl	C 514	11.2	53.3	30	5	PCT-US92-11357-21	Sequence 21, Appl
C 442	11.4	54.3	86	4	US-09-479-729B-23	Sequence 23, Appl	C 515	11.2	53.3	30	5	US-08-746-283-25	Sequence 25, Appl
C 443	11.4	54.3	86	4	US-09-257-179-3	Sequence 3, Appl	C 516	11.2	53.3	31	2	US-09-183-217-5	Sequence 5, Appl
C 444	11.4	54.3	86	4	US-09-149-476-3	Sequence 3, Appl	C 517	11.2	53.3	31	3	US-09-064-703-17	Sequence 17, Appl
C 445	11.4	54.3	86	4	US-09-288-143-3	Sequence 3, Appl	C 518	11.2	53.3	32	3	US-08-816-977-28	Sequence 28, Appl
C 446	11.4	54.3	86	4	US-09-487-792-25	Sequence 25, Appl	C 519	11.2	53.3	32	3	US-08-961-083-409	Sequence 409, App
C 447	11.4	54.3	86	4	US-09-152-060-3	Sequence 3, Appl	C 520	11.2	53.3	32	3	US-09-536-784-409	Sequence 4, Appl
C 448	11.4	54.3	86	4	US-09-908-594-25	Sequence 25, Appl	C 521	11.2	53.3	33	1	US-08-152-922A-1	Sequence 1, Appl
C 449	11.4	54.3	86	4	US-09-461-325-3	Sequence 3, Appl	C 522	11.2	53.3	33	1	US-08-479-723A-19	Sequence 19, Appl
C 450	11.4	54.3	86	4	US-09-489-847-3	Sequence 3, Appl	C 523	11.2	53.3	33	1	PCT-US94-04310-19	Sequence 19, Appl
C 451	11.4	54.3	86	4	US-09-231-788-18	Sequence 18, Appl	C 524	11.2	53.3	33	4	US-08-347-029-6	Sequence 6, Appl
C 452	11.4	54.3	86	4	US-09-512-363-19	Sequence 19, Appl	C 525	11.2	53.3	33	4	US-08-965-477-2	Sequence 5, Appl
C 453	11.4	54.3	86	4	US-09-176-200-19	Sequence 19, Appl	C 526	11.2	53.3	33	4	US-09-566-581-5	Sequence 5, Appl
C 454	11.4	54.3	86	4	US-09-202-258-3	Sequence 3, Appl	C 527	11.2	53.3	33	4	PCT-US95-14932-6	Sequence 6, Appl
C 455	11.4	54.3	86	4	US-09-690-454-3	Sequence 3, Appl	C 528	11.2	53.3	36	1	US-08-709-923-6	Sequence 6, Appl
C 456	11.4	54.3	86	4	US-09-482-271-11	Sequence 11, Appl	C 529	11.2	53.3	36	1	US-08-288-663A-5	Sequence 5, Appl
C 457	11.4	54.3	86	4	US-09-482-273-3	Sequence 3, Appl	C 530	11.2	53.3	36	1		
C 458	11.4	54.3	86	4	US-09-904-615-3	Sequence 3, Appl	C 531	11.2	53.3	36	1		
C 459	11.4	54.3	86	4	US-09-369-247-3	Sequence 3, Appl	C 532	11.2	53.3	36	1		
C 460	11.4	54.3	100	1	US-08-487-880A-119	Sequence 119, App	C 533	11.2	53.3	36	1		
C 461	11.4	54.3	100	1	US-08-478-435-119	Sequence 119, App	C 534	11.2	53.3	36	4		
C 462	11.4	54.3	100	2	US-08-337-463-119	Sequence 119, App	C 535	11.2	53.3	36	4		
C 463	11.4	54.3	100	2	US-08-478-373-119	Sequence 119, App	C 536	11.2	53.3	36	5		
C 464	11.4	54.3	100	2	US-08-474-671-119	Sequence 119, App	C 537	11.2	53.3	37	2		
C 465	11.4	54.3	100	3			C 538	11.2	53.3	37	2		

C 539	11.2	53.3	37	4	US-09-267-574-35	Sequence 35, Appl	C 612	11.2	53.3	71	3	US-08-471-039-140	Sequence 140, App
C 540	11.2	53.3	38	3	US-08-961-083-415	Sequence 415, App	C 613	11.2	53.3	71	4	US-08-559-390-159	Sequence 59, Appl
C 541	11.2	53.3	38	4	US-09-536-784-415	Sequence 415, App	C 614	11.2	53.3	71	4	US-08-559-390-140	Sequence 140, Appl
C 542	11.2	53.3	39	1	US-07-854-596B-58	Sequence 58, Appl	C 615	11.2	53.3	71	5	PCT-US93-11198-59	Sequence 59, Appl
C 543	11.2	53.3	39	1	US-07-854-596B-59	Sequence 59, Appl	C 616	11.2	53.3	71	5	PCT-US93-11198-140	Sequence 140, App
C 544	11.2	53.3	39	6	5498600-7	Patent No. 5498600	C 617	11.2	53.3	72	4	US-09-120-561C-10	Sequence 10, Appl
C 545	11.2	53.3	40	2	US-08-174-672D-22	Sequence 22, Appl	C 618	11.2	53.3	79	4	US-08-720-201A-10	Sequence 10, Appl
C 546	11.2	53.3	41	1	US-08-279-625A-6	Sequence 6, Appl	C 619	11.2	53.3	81	2	US-08-471-048-9	Sequence 9, Appl
C 547	11.2	53.3	45	2	US-08-432-693-5	Sequence 4, Appl	C 620	11.2	53.3	81	3	US-08-612-858-5	Sequence 5, Appl
C 548	11.2	53.3	45	2	US-08-642-406A-4	Sequence 4, Appl	C 621	11.2	53.3	81	3	US-08-137-032-9	Sequence 9, Appl
C 549	11.2	53.3	45	4	US-09-199-534-4	Sequence 4, Appl	C 622	11.2	53.3	83	1	US-08-093-741-19	Sequence 9, Appl
C 550	11.2	53.3	45	4	US-09-199-534-4	Sequence 4, Appl	C 623	11.2	53.3	83	1	US-08-093-741-13	Sequence 13, Appl
C 551	11.2	53.3	47	3	US-08-464-582-8	Sequence 8, Appl	C 624	11.2	53.3	83	1	US-08-720-012-9	Sequence 9, Appl
C 552	11.2	53.3	47	3	US-08-464-582-8	Sequence 8, Appl	C 625	11.2	53.3	83	1	US-08-720-012-13	Sequence 13, Appl
C 553	11.2	53.3	47	3	US-08-462-513-8	Sequence 8, Appl	C 626	11.2	53.3	83	2	US-08-560-098A-14	Sequence 14, Appl
C 554	11.2	53.3	47	3	US-08-462-513-9	Sequence 9, Appl	C 627	11.2	53.3	83	3	US-08-967-024C-8	Sequence 8, Appl
C 555	11.2	53.3	47	4	US-09-422-978-2964	Sequence 2964, Ap	C 628	11.2	53.3	84	4	US-09-397-787-13	Sequence 13, Appl
C 556	11.2	53.3	47	4	US-09-422-978-3290	Sequence 3290, Ap	C 629	11.2	53.3	89	1	US-08-411-796-141	Sequence 141, App
C 557	11.2	53.3	48	1	US-08-346-333-7	Sequence 7, Appl	C 630	11.2	53.3	89	1	US-08-411-796-142	Sequence 142, App
C 558	11.2	53.3	48	1	US-08-346-333-8	Sequence 8, Appl	C 631	11.2	53.3	89	1	US-08-411-796-143	Sequence 143, App
C 559	11.2	53.3	48	5	PCT-US91-07506-7	Sequence 7, Appl	C 632	11.2	53.3	89	1	US-08-411-796-157	Sequence 157, App
C 560	11.2	53.3	48	5	PCT-US91-07506-8	Sequence 8, Appl	C 633	11.2	53.3	89	1	US-08-411-796-157	Sequence 157, App
C 561	11.2	53.3	49	1	US-07-797-556-6	Sequence 6, Appl	C 634	11.2	53.3	89	1	US-08-411-796-158	Sequence 158, App
C 562	11.2	53.3	50	1	US-08-093-741-24	Sequence 24, Appl	C 635	11.2	53.3	89	3	US-08-471-039-141	Sequence 141, App
C 563	11.2	53.3	50	1	US-08-720-012-24	Sequence 24, Appl	C 636	11.2	53.3	89	3	US-08-471-039-142	Sequence 142, App
C 564	11.2	53.3	50	2	US-08-560-098A-29	Sequence 29, Appl	C 637	11.2	53.3	89	3	US-08-471-039-143	Sequence 143, App
C 565	11.2	53.3	50	3	US-08-967-024C-17	Sequence 17, Appl	C 638	11.2	53.3	89	3	US-08-471-039-157	Sequence 157, App
C 566	11.2	53.3	50	3	US-08-967-024C-17	Sequence 17, Appl	C 639	11.2	53.3	89	3	US-08-471-039-158	Sequence 158, App
C 567	11.2	53.3	50	4	US-09-546-934-25	Sequence 25, Appl	C 640	11.2	53.3	89	3	US-08-471-039-159	Sequence 159, App
C 568	11.2	53.3	51	1	US-07-936-163-33	Sequence 33, Appl	C 641	11.2	53.3	89	4	US-08-559-390-141	Sequence 141, App
C 569	11.2	53.3	51	1	US-08-729-601A-80	Sequence 80, Appl	C 642	11.2	53.3	89	4	US-08-559-390-142	Sequence 142, App
C 570	11.2	53.3	52	2	US-08-849-480A-22	Sequence 22, Appl	C 643	11.2	53.3	89	4	US-08-559-390-143	Sequence 143, App
C 571	11.2	53.3	53	1	US-08-411-796-119	Sequence 119, App	C 644	11.2	53.3	89	4	US-08-559-390-157	Sequence 157, App
C 572	11.2	53.3	53	1	US-08-411-796-120	Sequence 120, App	C 645	11.2	53.3	89	4	US-08-559-390-158	Sequence 158, App
C 573	11.2	53.3	53	1	US-08-411-796-121	Sequence 121, App	C 646	11.2	53.3	89	5	PCT-US93-11198-141	Sequence 141, App
C 574	11.2	53.3	53	1	US-08-411-796-122	Sequence 122, App	C 647	11.2	53.3	89	5	PCT-US93-11198-142	Sequence 142, App
C 575	11.2	53.3	53	1	US-08-411-796-123	Sequence 123, App	C 648	11.2	53.3	89	5	PCT-US93-11198-143	Sequence 143, App
C 576	11.2	53.3	53	3	US-08-471-039-119	Sequence 119, App	C 649	11.2	53.3	89	5	PCT-US93-11198-157	Sequence 157, App
C 577	11.2	53.3	53	3	US-08-471-039-120	Sequence 120, App	C 650	11.2	53.3	89	5	PCT-US93-11198-158	Sequence 158, App
C 578	11.2	53.3	53	3	US-08-471-039-121	Sequence 121, App	C 651	11.2	53.3	89	5	PCT-US93-11198-159	Sequence 159, App
C 579	11.2	53.3	53	3	US-08-471-039-122	Sequence 122, App	C 652	11.2	53.3	90	1	US-08-094-741A-4	Sequence 4, Appl
C 580	11.2	53.3	53	3	US-08-471-039-123	Sequence 123, App	C 653	11.2	53.3	91	1	US-08-093-741-10	Sequence 10, Appl
C 581	11.2	53.3	53	4	US-08-559-390-119	Sequence 119, App	C 654	11.2	53.3	91	1	US-08-093-741-14	Sequence 14, Appl
C 582	11.2	53.3	53	4	US-08-559-390-120	Sequence 120, App	C 655	11.2	53.3	91	1	US-08-093-741-14	Sequence 14, Appl
C 583	11.2	53.3	53	4	US-08-559-390-121	Sequence 121, App	C 656	11.2	53.3	91	1	US-08-720-012-10	Sequence 10, Appl
C 584	11.2	53.3	53	4	US-08-559-390-122	Sequence 122, App	C 657	11.2	53.3	91	1	US-08-720-012-14	Sequence 14, Appl
C 585	11.2	53.3	53	4	US-08-559-390-123	Sequence 123, App	C 658	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 586	11.2	53.3	53	5	PCT-US93-11198-119	Sequence 119, App	C 659	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 587	11.2	53.3	53	5	PCT-US93-11198-120	Sequence 120, App	C 660	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 588	11.2	53.3	53	5	PCT-US93-11198-121	Sequence 121, App	C 661	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 589	11.2	53.3	53	5	PCT-US93-11198-122	Sequence 122, App	C 662	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 590	11.2	53.3	53	5	PCT-US93-11198-123	Sequence 123, App	C 663	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 591	11.2	53.3	57	2	US-08-612-858-96	Sequence 36, Appl	C 664	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 592	11.2	53.3	57	2	US-08-612-858-96	Sequence 36, Appl	C 665	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 593	11.2	53.3	58	1	US-08-093-741-18	Sequence 18, Appl	C 666	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 594	11.2	53.3	58	1	US-08-093-741-18	Sequence 18, Appl	C 667	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 595	11.2	53.3	58	1	US-08-093-741-18	Sequence 18, Appl	C 668	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 596	11.2	53.3	58	2	US-08-560-098A-19	Sequence 19, Appl	C 669	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 597	11.2	53.3	58	2	US-08-560-098A-19	Sequence 19, Appl	C 670	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 598	11.2	53.3	58	3	US-09-003-903-4	Sequence 4, Appl	C 671	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 599	11.2	53.3	60	3	US-09-344-510B-33	Sequence 33, Appl	C 672	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 600	11.2	53.3	63	2	US-08-974-549A-720	Sequence 720, Appl	C 673	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 601	11.2	53.3	63	3	US-08-560-098A-37	Sequence 37, Appl	C 674	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 602	11.2	53.3	63	3	US-08-967-024C-22	Sequence 22, Appl	C 675	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 603	11.2	53.3	64	6	US-08-967-024C-23	Sequence 23, Appl	C 676	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 604	11.2	53.3	69	1	5422249-12	Patent No. 5422249	C 677	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 605	11.2	53.3	70	1	US-08-242-098-35	Sequence 35, Appl	C 678	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 606	11.2	53.3	70	1	US-08-093-741-20	Sequence 20, Appl	C 679	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 607	11.2	53.3	70	1	US-08-720-012-20	Sequence 20, Appl	C 680	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 608	11.2	53.3	70	2	US-08-560-098A-21	Sequence 21, Appl	C 681	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 609	11.2	53.3	71	1	US-08-967-024C-13	Sequence 13, Appl	C 682	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 610	11.2	53.3	71	1	US-08-411-796-59	Sequence 59, Appl	C 683	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 611	11.2	53.3	71	3	US-08-411-796-140	Sequence 140, Appl	C 684	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 612	11.2	53.3	71	3	US-08-471-039-59	Sequence 59, Appl	C 685	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl

C 685	11	52.4	29	1	US-08-105-483-417	Sequence 417, App	C 758	11	52.4	56	3	US-08-928-213B-103	Sequence 103, App
C 686	11	52.4	29	1	US-08-709-209-417	Sequence 417, App	C 759	11	52.4	56	3	US-08-928-213B-104	Sequence 104, App
C 687	11	52.4	29	1	US-08-303-275-125	Sequence 125, App	C 760	11	52.4	60	1	US-08-210-222-37	Sequence 37, App
C 688	11	52.4	29	1	US-08-458-101-417	Sequence 417, App	C 761	11	52.4	60	3	US-08-872-056-10	Sequence 10, App
C 689	11	52.4	29	3	US-08-779-764A-64	Sequence 64, App	C 762	11	52.4	61	3	US-09-046-24-26	Sequence 26, App
C 690	11	52.4	29	4	US-08-851-120-4	Sequence 4, App	C 763	11	52.4	61	3	US-07-977-284A-192	Sequence 192, App
C 691	11	52.4	30	4	US-09-019-793A-108	Sequence 108, App	C 764	11	52.4	66	2	US-08-256-426B-192	Sequence 192, App
C 692	11	52.4	30	4	US-09-860-793-21	Sequence 21, App	C 765	11	52.4	67	2	US-08-464-073-11	Sequence 11, App
C 693	11	52.4	31	2	US-08-577-492-7	Sequence 7, App	C 766	11	52.4	67	2	US-07-814-220-16	Sequence 16, App
C 694	11	52.4	31	2	US-09-079-630-7	Sequence 7, App	C 767	11	52.4	67	2	US-07-814-220-17	Sequence 17, App
C 695	11	52.4	32	2	US-08-859-998-425	Sequence 425, App	C 768	11	52.4	67	2	US-07-812-421-16	Sequence 16, App
C 696	11	52.4	32	2	US-09-925-928-425	Sequence 425, App	C 769	11	52.4	67	2	US-08-428-252-11	Sequence 11, App
C 697	11	52.4	32	4	US-09-225-201B-425	Sequence 425, App	C 770	11	52.4	67	2	US-08-416-516A-11	Sequence 11, App
C 698	11	52.4	33	1	US-08-245-754A-4	Sequence 4, App	C 771	11	52.4	68	3	US-09-081-180-34	Sequence 34, App
C 699	11	52.4	33	1	US-08-485-602-26	Sequence 26, App	C 772	11	52.4	68	3	US-09-040-786-34	Sequence 34, App
C 700	11	52.4	33	1	US-08-757-180-25	Sequence 25, App	C 773	11	52.4	87	1	US-08-433-126A-73	Sequence 73, App
C 701	11	52.4	33	1	US-08-745-638-26	Sequence 26, App	C 774	11	52.4	87	1	US-08-433-124A-73	Sequence 73, App
C 702	11	52.4	33	2	US-08-597-731-4	Sequence 4, App	C 775	11	52.4	87	1	US-08-976-413A-73	Sequence 73, App
C 703	11	52.4	34	1	US-07-955-041-5	Sequence 5, App	C 776	11	52.4	87	5	PCT-US96-06059-73	Sequence 35, App
C 704	11	52.4	34	1	US-08-227-455-5	Sequence 5, App	C 777	11	52.4	93	2	US-08-771-201-6	Sequence 6, App
C 705	11	52.4	34	1	US-08-472-482-5	Sequence 5, App	C 778	11	52.4	94	2	US-08-210-222-35	Sequence 29, App
C 706	11	52.4	34	1	US-08-487-069-5	Sequence 5, App	C 779	11	52.4	96	5	PCT-US94-06456-29	Sequence 58, App
C 707	11	52.4	34	3	US-09-232-477-13	Sequence 13, App	C 780	11	52.4	96	5	PCT-US94-06456-58	Sequence 15, App
C 708	11	52.4	34	4	US-09-784-982-13	Sequence 13, App	C 781	11	52.4	97	1	US-08-210-222-15	Sequence 5, App
C 709	11	52.4	36	1	US-08-316-293-52	Sequence 52, App	C 782	11	52.4	98	1	US-08-210-222-3	Sequence 8, App
C 710	11	52.4	36	3	US-09-213-053-18	Sequence 18, App	C 783	11	52.4	98	1	US-08-210-222-5	Sequence 23, App
C 711	11	52.4	38	2	US-08-709-874A-28	Sequence 28, App	C 784	11	52.4	98	1	US-08-210-222-8	Sequence 26, App
C 712	11	52.4	38	3	US-09-104-382-28	Sequence 28, App	C 785	11	52.4	98	1	US-08-210-222-23	Sequence 26, App
C 713	11	52.4	39	3	US-09-772-342B-4	Sequence 4, App	C 786	11	52.4	98	1	US-08-210-222-28	Sequence 28, App
C 714	11	52.4	39	4	US-09-693-147-18	Sequence 18, App	C 787	11	52.4	98	1	US-08-487-890A-118	Sequence 118, App
C 715	11	52.4	40	1	US-08-210-222-39	Sequence 39, App	C 788	11	52.4	99	1	US-08-478-435-118	Sequence 118, App
C 716	11	52.4	40	3	US-09-306-290-21	Sequence 21, App	C 789	11	52.4	99	2	US-08-377-483-118	Sequence 118, App
C 717	11	52.4	42	3	US-08-969-815-29	Sequence 29, App	C 790	11	52.4	99	2	US-08-478-373-118	Sequence 118, App
C 718	11	52.4	42	3	US-09-120-025-29	Sequence 29, App	C 791	11	52.4	99	2	US-08-474-671-118	Sequence 118, App
C 719	11	52.4	42	4	US-09-710-481-29	Sequence 29, App	C 792	11	52.4	99	3	US-08-897-654-118	Sequence 118, App
C 720	11	52.4	42	4	US-09-553-875-29	Sequence 29, App	C 793	11	52.4	99	3	US-08-637-654-118	Sequence 118, App
C 721	11	52.4	42	4	US-09-768-670-29	Sequence 29, App	C 794	11	52.4	99	4	US-08-637-654-118	Sequence 118, App
C 722	11	52.4	43	1	US-08-210-222-36	Sequence 36, App	C 795	11	52.4	99	4	US-08-649-518-118	Sequence 118, App
C 723	11	52.4	43	4	US-09-393-007-2	Sequence 2, App	C 796	11	52.4	99	4	US-08-411-796-391	Sequence 391, App
C 724	11	52.4	44	1	US-08-171-389-129	Sequence 129, App	C 797	11	52.4	18	1	US-08-411-796-393	Sequence 393, App
C 725	11	52.4	44	1	US-08-123-936-129	Sequence 129, App	C 798	10.8	51.4	18	1	US-08-411-796-395	Sequence 395, App
C 726	11	52.4	44	2	US-08-475-228A-129	Sequence 129, App	C 799	10.8	51.4	18	1	US-08-411-796-397	Sequence 397, App
C 727	11	52.4	44	2	US-08-658-665-169	Sequence 169, App	C 800	10.8	51.4	18	1	US-08-411-796-397	Sequence 397, App
C 728	11	52.4	44	3	US-08-482-080A-129	Sequence 129, App	C 801	10.8	51.4	18	1	US-08-411-796-399	Sequence 399, App
C 729	11	52.4	44	3	US-08-796-101-145	Sequence 145, App	C 802	10.8	51.4	18	1	US-08-411-796-399	Sequence 399, App
C 730	11	52.4	44	3	US-09-376-097-16	Sequence 16, App	C 803	10.8	51.4	18	1	US-08-411-796-401	Sequence 401, App
C 731	11	52.4	44	3	US-09-085-273-169	Sequence 169, App	C 804	10.8	51.4	18	1	US-08-411-796-405	Sequence 405, App
C 732	11	52.4	44	4	US-09-354-947-129	Sequence 129, App	C 805	10.8	51.4	18	1	US-08-411-796-407	Sequence 407, App
C 733	11	52.4	44	5	PCT-US93-12388-129	Sequence 129, App	C 806	10.8	51.4	18	1	US-08-411-796-409	Sequence 409, App
C 734	11	52.4	45	2	US-08-642-406A-7	Sequence 7, App	C 807	10.8	51.4	18	1	US-08-411-796-541	Sequence 541, App
C 735	11	52.4	45	4	US-09-199-534-7	Sequence 7, App	C 808	10.8	51.4	18	2	US-09-205-204-35	Sequence 35, App
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C 737	11	52.4	46	3	US-08-258-287B-17	Sequence 17, App	C 810	10.8	51.4	18	3	US-08-471-039-393	Sequence 393, App
C 738	11	52.4	46	3	US-08-368-704C-17	Sequence 17, App	C 811	10.8	51.4	18	3	US-08-471-039-395	Sequence 395, App
C 739	11	52.4	47	4	US-09-671-317-633	Sequence 633, App	C 812	10.8	51.4	18	3	US-08-471-039-397	Sequence 397, App
C 740	11	52.4	47	4	US-09-422-978-87	Sequence 87, App	C 813	10.8	51.4	18	3	US-08-471-039-399	Sequence 399, App
C 741	11	52.4	47	4	US-09-422-978-635	Sequence 635, App	C 814	10.8	51.4	18	3	US-08-471-039-401	Sequence 401, App
C 742	11	52.4	47	4	US-09-422-978-1128	Sequence 1128, App	C 815	10.8	51.4	18	3	US-08-471-039-403	Sequence 403, App
C 743	11	52.4	47	4	US-09-422-978-1644	Sequence 1644, App	C 816	10.8	51.4	18	3	US-08-471-039-405	Sequence 405, App
C 744	11	52.4	47	4	US-09-422-978-2871	Sequence 2871, App	C 817	10.8	51.4	18	3	US-08-471-039-407	Sequence 407, App
C 745	11	52.4	47	4	US-09-422-978-3297	Sequence 3297, App	C 818	10.8	51.4	18	3	US-08-471-039-409	Sequence 409, App
C 746	11	52.4	47	4	US-09-422-978-3399	Sequence 3399, App	C 819	10.8	51.4	18	3	US-08-471-039-441	Sequence 441, App
C 747	11	52.4	48	1	US-08-210-222-38	Sequence 38, App	C 820	10.8	51.4	18	4	US-08-559-390-391	Sequence 391, App
C 748	11	52.4	48	3	US-08-952-457-7	Sequence 7, App	C 821	10.8	51.4	18	4	US-08-559-390-393	Sequence 393, App
C 749	11	52.4	49	3	US-08-651-472-70	Sequence 70, App	C 822	10.8	51.4	18	4	US-08-559-390-395	Sequence 395, App
C 750	11	52.4	49	3	US-08-358-928-70	Sequence 70, App	C 823	10.8	51.4	18	4	US-08-559-390-397	Sequence 397, App
C 751	11	52.4	49	4	US-08-897-956A-31	Sequence 31, App	C 824	10.8	51.4	18	4	US-08-559-390-399	Sequence 399, App
C 752	11	52.4	50	2	US-08-818-604-11	Sequence 11, App	C 825	10.8	51.4	18	4	US-08-559-390-401	Sequence 401, App
C 753	11	52.4	50	2	US-08-381-637-7	Sequence 7, App	C 826	10.8	51.4	18	4	US-08-559-390-403	Sequence 403, App
C 754	11	52.4	50	4	US-09-410-903-83	Sequence 83, App	C 827	10.8	51.4	18	4	US-08-559-390-405	Sequence 405, App
C 755	11	52.4	50	4	US-09-346-946-11	Sequence 11, App	C 828	10.8	51.4	18	4	US-08-559-390-407	Sequence 407, App
C 756	11	52.4	51	3	US-08-832-985-2	Sequence 2, App	C 829	10.8	51.4	18	4	US-08-559-390-409	Sequence 409, App
C 757	11	52.4	51	4	US-08-835-159-2	Sequence 2, App	C 830	10.8	51.4	18	4	US-08-559-390-409	Sequence 409, App

831	10.8	51.4	18	4	US-08-559-390-541	Sequence 541, App	C 904	10.8	51.4	35	1	US-08-411-796-57	Sequence 57, App
832	10.8	51.4	18	5	PCT-US93-11198-391	Sequence 391, App	C 905	10.8	51.4	35	1	US-08-207-481-36	Sequence 36, App
833	10.8	51.4	18	5	PCT-US93-11198-393	Sequence 393, App	C 906	10.8	51.4	35	3	US-08-411-039-57	Sequence 57, App
834	10.8	51.4	18	5	PCT-US93-11198-395	Sequence 395, App	C 907	10.8	51.4	35	3	US-08-559-390-57	Sequence 57, App
835	10.8	51.4	18	5	PCT-US93-11198-397	Sequence 397, App	C 908	10.8	51.4	35	5	PCT-US93-11198-57	Sequence 57, App
836	10.8	51.4	18	5	PCT-US93-11198-399	Sequence 399, App	C 909	10.8	51.4	35	5	PCT-US93-11198-38	Sequence 38, App
837	10.8	51.4	18	5	PCT-US93-11198-401	Sequence 401, App	C 910	10.8	51.4	35	5	PCT-US93-11198-42	Sequence 42, App
838	10.8	51.4	18	5	PCT-US93-11198-403	Sequence 403, App	C 911	10.8	51.4	35	5	PCT-US93-11198-45	Sequence 45, App
839	10.8	51.4	18	5	PCT-US93-11198-405	Sequence 405, App	C 912	10.8	51.4	36	3	US-09-183-217-4	Sequence 4, App
840	10.8	51.4	18	5	PCT-US93-11198-407	Sequence 407, App	C 913	10.8	51.4	36	4	US-09-424-6208-7	Sequence 7, App
841	10.8	51.4	18	5	PCT-US93-11198-409	Sequence 409, App	C 914	10.8	51.4	36	4	US-09-424-6208-12	Sequence 12, App
842	10.8	51.4	18	5	PCT-US93-11198-411	Sequence 411, App	C 915	10.8	51.4	36	4	US-09-424-6208-17	Sequence 17, App
843	10.8	51.4	19	2	US-08-852-407-4	Sequence 4, App	C 916	10.8	51.4	39	1	US-08-447-422-4	Sequence 2, App
844	10.8	51.4	20	3	US-08-485-942A-84	Sequence 84, App	C 917	10.8	51.4	39	1	US-08-484-192-17	Sequence 17, App
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846	10.8	51.4	20	3	US-08-488-208A-84	Sequence 84, App	C 919	10.8	51.4	40	3	US-08-996-441B-77	Sequence 77, App
847	10.8	51.4	20	3	US-09-021-701-962	Sequence 962, App	C 920	10.8	51.4	40	3	US-08-993-722A-77	Sequence 77, App
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852	10.8	51.4	20	3	US-09-021-701-967	Sequence 967, App	C 925	10.8	51.4	40	3	US-09-570-214B-17	Sequence 17, App
853	10.8	51.4	20	3	US-09-021-701-968	Sequence 968, App	C 926	10.8	51.4	41	2	US-08-614-686A-14	Sequence 14, App
854	10.8	51.4	20	4	US-08-483-211A-84	Sequence 84, App	C 927	10.8	51.4	42	1	US-08-399-696-56	Sequence 56, App
855	10.8	51.4	20	4	US-08-564-805-84	Sequence 84, App	C 928	10.8	51.4	43	2	US-08-882-083-14	Sequence 14, App
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863	10.8	51.4	21	4	US-09-564-805-83	Sequence 83, App	C 936	10.8	51.4	47	4	US-08-614-638-1037	Sequence 1037, App
864	10.8	51.4	21	4	US-08-949-344C-40	Sequence 40, App	C 937	10.8	51.4	47	4	US-09-422-978-804	Sequence 804, App
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866	10.8	51.4	23	1	US-08-465-590-98	Sequence 98, App	C 939	10.8	51.4	47	4	US-09-422-978-2558	Sequence 2558, App
867	10.8	51.4	23	3	US-09-184-658-22	Sequence 22, App	C 940	10.8	51.4	47	4	US-09-854-302-1	Sequence 1, App
868	10.8	51.4	23	3	US-08-711-417C-98	Sequence 98, App	C 941	10.8	51.4	48	1	US-07-826-928A-18	Sequence 18, App
869	10.8	51.4	23	5	PCT-US93-08743-98	Sequence 98, App	C 942	10.8	51.4	50	4	US-08-449-567A-95	Sequence 95, App
870	10.8	51.4	24	1	US-08-411-796-202	Sequence 202, App	C 943	10.8	51.4	53	1	US-08-411-796-124	Sequence 124, App
871	10.8	51.4	24	3	US-08-411-039-202	Sequence 202, App	C 944	10.8	51.4	53	3	US-08-471-039-124	Sequence 124, App
872	10.8	51.4	24	4	US-08-559-390-202	Sequence 202, App	C 945	10.8	51.4	53	4	US-09-570-214B-21	Sequence 21, App
873	10.8	51.4	24	5	PCT-US93-11198-202	Sequence 202, App	C 946	10.8	51.4	53	5	US-08-559-390-124	Sequence 124, App
874	10.8	51.4	27	2	US-08-839-306-1	Sequence 1, App	C 947	10.8	51.4	53	4	PCT-US93-11198-124	Sequence 124, App
875	10.8	51.4	27	4	US-09-602-586-49	Sequence 49, App	C 948	10.8	51.4	56	1	US-08-213-811-5	Sequence 5, App
876	10.8	51.4	28	1	US-08-629-939-12	Sequence 12, App	C 949	10.8	51.4	60	1	US-08-109-934-18	Sequence 18, App
877	10.8	51.4	28	1	US-08-759-873-12	Sequence 12, App	C 950	10.8	51.4	60	2	US-08-764-575-18	Sequence 18, App
878	10.8	51.4	29	1	US-08-346-455B-62	Sequence 62, App	C 951	10.8	51.4	68	1	US-08-208-886C-51	Sequence 51, App
879	10.8	51.4	29	1	US-08-207-481-15	Sequence 15, App	C 952	10.8	51.4	68	1	US-08-704-744-51	Sequence 51, App
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881	10.8	51.4	29	3	US-09-483-831B-62	Sequence 62, App	C 954	10.8	51.4	68	2	US-08-290-793B-51	Sequence 51, App
882	10.8	51.4	29	4	PCT-US95-02689-15	Sequence 15, App	C 955	10.8	51.4	68	2	US-08-284-516C-25	Sequence 25, App
883	10.8	51.4	29	5	PCT-US95-06611-62	Sequence 62, App	C 956	10.8	51.4	70	1	US-09-537-911A-25	Sequence 25, App
884	10.8	51.4	30	1	US-08-627-845-6	Sequence 6, App	C 957	10.8	51.4	70	1	US-08-257-073-47	Sequence 47, App
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886	10.8	51.4	30	1	US-08-207-481-23	Sequence 23, App	C 959	10.8	51.4	70	3	US-08-796-101-158	Sequence 154, App
887	10.8	51.4	30	2	US-08-666-405-20	Sequence 20, App	C 960	10.6	50.5	17	1	US-08-773-124A-728	Sequence 728, App
888	10.8	51.4	30	2	US-08-882-649A-18	Sequence 18, App	C 961	10.6	50.5	17	1	US-08-435-628-728	Sequence 728, App
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890	10.8	51.4	30	4	PCT-US95-02689-23	Sequence 23, App	C 963	10.6	50.5	20	2	US-08-670-707A-34	Sequence 34, App
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892	10.8	51.4	31	2	US-08-816-155B-24	Sequence 24, App	C 965	10.6	50.5	20	3	US-09-435-296-63	Sequence 63, App
893	10.8	51.4	31	3	US-09-033-055A-7	Sequence 7, App	C 966	10.6	50.5	20	3	US-09-037-601-34	Sequence 34, App
894	10.8	51.4	31	3	US-09-079-587-24	Sequence 24, App	C 967	10.6	50.5	20	4	US-08-899-241-252	Sequence 252, App
895	10.8	51.4	32	3	US-08-938-830-18	Sequence 18, App	C 968	10.6	50.5	20	4	US-09-315-179-34	Sequence 34, App
896	10.8	51.4	32	3	US-09-020-222-18	Sequence 18, App	C 969	10.6	50.5	20	4	US-09-780-175-105	Sequence 105, App
897	10.8	51.4	32	3	US-09-529-279-37	Sequence 37, App	C 970	10.6	50.5	20	4	US-09-853-768-69	Sequence 69, App
898	10.8	51.4	32	3	US-10-158-885-37	Sequence 37, App	C 971	10.6	50.5	20	4	US-09-853-656-26	Sequence 26, App
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900	10.8	51.4	33	1	US-08-257-073-114	Sequence 114, App	C 973	10.6	50.5	20	4	US-09-198-452A-5313	Sequence 5313, App
901	10.8	51.4	33	3	US-08-169-715-15	Sequence 15, App	C 974	10.6	50.5	21	1	US-08-211-430-11	Sequence 11, App
902	10.8	51.4	33	4	US-08-169-715-15	Sequence 15, App	C 975	10.6	50.5	21	3	US-07-998-289B-22	Sequence 22, App
903	10.8	51.4	33	5	PCT-US92-00731-10	Sequence 10, App	C 976	10.6	50.5	21	3	US-09-174-437-45	Sequence 45, App

US-09-744-875a-1.max.rml

Sequence 45, Appl
Sequence 4, Appl
Sequence 24, Appl
Sequence 522, Appl
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Sequence 21, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 3, Appl
Sequence 8, Appl
Sequence 5, Appl
Patent No. 5231168
Sequence 704, Appl
Sequence 84, Appl
Sequence 44, Appl
Sequence 8, Appl
Sequence 17, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 44, Appl
Sequence 17, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-08-366-276-8

Sequence 8, Application US/08366276

Patent No. 5534409

GENERAL INFORMATION:

APPLICANT: Groner, Bernd

APPLICANT: Gouilleux, Fabrice

APPLICANT: Makao, Hiroshi

TITLE OF INVENTION: Cytokine Regulated Transcription Factor

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/366,276

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9409396.0

FILING DATE: 11-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Elmer, James Scott

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: 4-19992/A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "MGF binding sequence from

DESCRIPTION: bovine b-casein"

HYPOTHETICAL: NO

US-08-366-276-8

Query Match 85.7%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 1 AGATTCTAGGAATTCAA 18

RESULT 2

US-09-522-217-59

Sequence 59, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:

APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

CURRENT FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: US 60/123,904

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: US 60/142,013

EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 59

LENGTH: 100

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide ZC12749

US-09-522-217-59

Query Match 85.7%; Score 18; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 67 AGATTCTAGGAATTCAA 84

RESULT 3

US-09-522-217-60/C

Sequence 60, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:

APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI LIGAND

FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 100
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC12748
US-09-522-217-60

Query Match 85.7%; Score 18; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
Db 38 AGATTCTAGGAATTCAA 21

RESULT 4
US-08-369-754-1/c
Sequence 1, Application US/08369754
Patent No. 6537553
GENERAL INFORMATION:
APPLICANT: FUKUDA, MINORU
APPLICANT: SAWADA, RITSUKO
APPLICANT: TSUBOI, SHIGERU
TITLE OF INVENTION: E-SELECTIN-DEPENDENT CELL ADHESION
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE. 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,754
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1113
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-369-754-1

Query Match 73.3%; Score 15.4; DB 4; Length 24;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATTCTAGCAATTCAA 19
Db 17 ATTCTAGCAATTCAA 1

RESULT 5
US-09-140-804-46
Sequence 46, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 46
LENGTH: 58
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC14819
US-09-140-804-46

Query Match 69.5%; Score 14.6; DB 3; Length 58;
Best Local Similarity 81.0%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAATC 21
Db 14 AGAATCTAGGAATTCATTC 34

RESULT 6
US-09-173-043-22
Sequence 22, Application US/09173043
Patent No. 6207442
GENERAL INFORMATION:
APPLICANT: Raymond, Christopher K.
TITLE OF INVENTION: PLASMID CONSTRUCTION BY HOMOLOGOUS
FILE REFERENCE: 97-27
CURRENT APPLICATION NUMBER: US/09/173,043
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: US 60/062,061
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 58
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-09-173-043-22

Query Match 69.5%; Score 14.6; DB 3; Length 58;
Best Local Similarity 81.0%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAATC 21
Db 14 AGAATCTAGGAATTCATTC 34

RESULT 7
US-09-209-525-42
Sequence 42, Application US/09209525

```

? Patent No. 6303770
?
? GENERAL INFORMATION:
?
? APPLICANT: Iok, Si
?
? APPLICANT: Conklin, Darrell C.
?
? APPLICANT: Parrish, Julia E.
?
? TITLE OF INVENTION: Mammalian Alpha Helical Protein-1
?
? FILE REFERENCE: 97-71
?
? CURRENT APPLICATION NUMBER: US/09/209,525
?
? CURRENT FILING DATE: 1998-12-10
?
? NUMBER OF SEQ ID NOS: 56
?
? SOFTWARE: FastSeq for Windows Version 3.0
?
? SEQ ID NO 42
?
? LENGTH: 58
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
US-09-209-525-42

```

Query Match	14.6;	Score	14.6;	DB 4;	Length	58;	
Best Local Similarity	81.0%;	Pred. No.	4.2E+02;				
Matches	17;	Conservative	0;	Mismatches	4;	Indels	0;
						Gaps	0;

```

QY      1 AGATTCTAGGAATCAATC 21
        ||| ||||| ||| |||
Db      14 AGATACTAGGAATCTACTC 34

```

```

RESULT 8
US-09-686-838B-46
/ Sequence 46, Application US/09686838B
/ Patent No. 6482612
/ GENERAL INFORMATION:
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Humes, Jacqueline M.
/ TITLE OF INVENTION: Adipocyte-Specific Protein Homologs
/ FILE REFERENCE: 97-49D1
/ CURRENT APPLICATION NUMBER: US/09/686,838B
/ CURRENT FILING DATE: 2000-10-10
/ PRIOR APPLICATION NUMBER: US 03/140,804
/ PRIOR FILING DATE: 1998-08-26
/ PRIOR APPLICATION NUMBER: US 60/056,383
/ PRIOR FILING DATE: 1997-08-26
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 46
/ LENGTH: 58
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide ZC14819
US-09-686-838B-46

```

Query Match	69.5%;	Score 14.6;	DB 4;	Length 58;
Best Local Similarity	81.0%;	Pred. No. 4.2e+02;		
Matches 17; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

```

QY      1 AGATTCTAGGAATTCAAATC 21
          ||| | | | | | | | | |
Db      14 AGAATACTAGGAATTCATTC 34

```

RESULT 9
US-09-662-402A-35/c
; Sequence 35, Application US/09662402A
; Patent No. 6420117
; GENERAL INFORMATION:
; APPLICANT: Messler, Susan R
; APPLICANT: Casa, Alexandra M
; TITLE OF INVENTION: MINIATURE INVERTED REPEAT TRANSPOSABLE ELEMENTS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 235,00230101
; CURRENT APPLICATION NUMBER: US/09/662,402A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/153,812
;

```

? PRIOR FILING DATE: 1999-09-14
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 35
? LENGTH: 20
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence
? OTHER INFORMATION: Oligonucleotide primer
US-09-662-402A-35

```

Query Match	67.6%;	DB 4;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 6e+02;	
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;
			Gaps 0;

QY 3 ATTTCTAGGAATTC AATC 21
 |||||
 Db 19 ATTTGAGGAATTGGAATC 1

RESULT 10
 US-08-201-697-12/C
 Sequence 12, Application US/08201697
 Patent No. 5705623
 GENERAL INFORMATION:
 APPLICANT: Wiggins, Roger C.
 APPLICANT: Thomas, Peedikayil E.
 TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
 TITLE OF INVENTION: 1
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentm Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/201,697
 FILING DATE: 25-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-0M 9783
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

Query Match	65.7%	Score 13.8	DB 1	length 30
Best Local Similarity	88.2%	Pred. No. 9.4e+02		
Matches 15; Conservative	0	Mismatches 2	Indels 0	Gaps 0

QY 3 ATTTCTAGGAATCAAA 15
| | | | | | | | | |
Db 17 AGTCCTAGGAATTC AAA 1

RESULT 11
US-08-463-090B-24/c

Sequence 24, Application US/08463090B
Patent No. 5801015
GENERAL INFORMATION:
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
APPLICANT: Draetta, Gullio
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
NUMBER OF INVENTIONS: Human Pathogens, and Uses Related Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot, LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,090B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV032.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-08-463-090B-24

Query Match 65.7%; Score 13.8; DB 1; Length 30;
Best Local Similarity 88.2%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAA 19
DB 20 ATTACTATGAATTCAAA 4

RESULT 12
US-08-332-420-54/c
Sequence 54, Application US/08332420
Patent No. 5744300
GENERAL INFORMATION:
APPLICANT: Maarten H.K. Linckens, et al.
TITLE OF INVENTION: METHODS AND REAGENTS FOR THE
IDENTIFICATION AND REGULATION
NUMBER OF INVENTIONS: OF SENESENCE-RELATED GENES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,420
FILING DATE: October 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,180
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Waidburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 34
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-332-420-54

Query Match 64.8%; Score 13.6; DB 1; Length 34;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20
DB 32 AGAGATCGAAGATTCAAAT 13

RESULT 13
US-07-941-363-1
Sequence 1, Application US/07941363
Patent No. 5348886
GENERAL INFORMATION:
APPLICANT: Lee, Stephen C.
APPLICANT: Luckow, Verne A.
APPLICANT: Leusch, Mark S.
APPLICANT: Olin, Peter O.
TITLE OF INVENTION: Method of Producing Recombinant
NUMBER OF INVENTIONS: Eukaryotic Viruses in Bacteria
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,363
FILING DATE: 19920904
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 07-21 (872) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 694-5402
TELEFAX: (314) 694-9009
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-07-941-363-1

Query Match 64.8%; Score 13.6; DB 1; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20
DB 1 AGATTCTAGGAATTCACAT 20

RESULT 14

US-09-143-634-28/c
Sequence 28, Application US/09143634
Patent No. 6214602
GENERAL INFORMATION:
APPLICANT: Zdanovsky, Alexey G.
TITLE OF INVENTION: EXPRESSION OF CLOSTRIDIAL TOXINS AND PROTEINS
FILE REFERENCE: PRMG-03193
CURRENT APPLICATION NUMBER: US/09/143,634
CURRENT FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 38
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-143-634-28

Query Match 64.8%; Score 13.6; DB 3; Length 38;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GATTCTAGGAATTCAAATC 21
DB 21 GATTCTAGGAATTCAGATC 2

RESULT 15

US-08-308-196A-4
Sequence 4, Application US/08308196A
Patent No. 5612198
GENERAL INFORMATION:
APPLICANT: Briereley, Russell A.
APPLICANT: Davis, Geneva R.
APPLICANT: Holtz, Gregory C.
APPLICANT: Gleeson, Martin A.
APPLICANT: Howard, Bradley D.
TITLE OF INVENTION: Production of Insulin-Like Growth
TITLE OF INVENTION: Factor-1 in Methylotrophic Yeast Cells
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,196A
FILING DATE: 09-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,523
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/578,728

FILING DATE: 04-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 51875
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic DNA)
US-08-308-196A-4

Query Match 64.8%; Score 13.6; DB 1; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20
DB 5 AGCTTGATAGGAATTCAAAT 24

RESULT 16

US-09-289-803-3
Sequence 3, Application US/09289803
Patent No. 6162605
GENERAL INFORMATION:
APPLICANT: Fort, Thomas L.
APPLICANT: McMillian, Ray A.
APPLICANT: Hellyer, Tobin
APPLICANT: You, Otimin
TITLE OF INVENTION: Amplification and Detection of Shiga-Like Toxin I
TITLE OF INVENTION: Producing Organisms
FILE REFERENCE: SLT-1 Application
CURRENT APPLICATION NUMBER: US/09/289,803
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer for SDA
US-09-289-803-3

Query Match 64.8%; Score 13.6; DB 3; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20
DB 13 AGACTTCTCGGATTCACAT 32

RESULT 17

PCT-US91-06452-4
Sequence 4, Application PC/TUS9106452
GENERAL INFORMATION:
APPLICANT: Briereley, Russell A.
APPLICANT: Davis, Geneva R.
APPLICANT: Holtz, Gregory C.
APPLICANT: Gleeson, Martin A.
APPLICANT: Bradley, D. H.
TITLE OF INVENTION: Production of Insulin-Like Growth
TITLE OF INVENTION: Factor-1 in Methylotrophic Yeast Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSER: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06452
FILING DATE: 19910409
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/578,728
FILING DATE: 04-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 51874
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PCT-US91-06452-4

Query Match 64.8%; Score 13.6; DB 5; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20
DB 5 AGCTTGATAGGAATTCAAAT 24

RESULT 18
US-09-289-803-2
Sequence 2, Application US/09289803
Patent No. 6162605
GENERAL INFORMATION:
APPLICANT: Fort, Thomas L.
APPLICANT: McMillian, Ray A.
APPLICANT: Hellyer, Tobin
APPLICANT: You, Qimin
TITLE OF INVENTION: Amplification and Detection of Shiga-like Toxin I
FILE REFERENCE: SLT-I Application
CURRENT APPLICATION NUMBER: US/09/289,803
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 41
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer for SDA
OTHER INFORMATION: of SLT-I Producing Organisms
US-09-289-803-2

Query Match 64.8%; Score 13.6; DB 3; Length 41;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20

DB 13 AGACTTCGCGAATTCACAT 32

RESULT 19
US-09-289-803-1
Sequence 1, Application US/09289803
Patent No. 6162605
GENERAL INFORMATION:
APPLICANT: Fort, Thomas L.
APPLICANT: McMillian, Ray A.
APPLICANT: Hellyer, Tobin
APPLICANT: You, Qimin
TITLE OF INVENTION: Amplification and Detection of Shiga-like Toxin I
FILE REFERENCE: SLT-I Application
CURRENT APPLICATION NUMBER: US/09/289,803
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 42
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer for SDA
OTHER INFORMATION: of SLT-I Producing Organisms
US-09-289-803-1

Query Match 64.8%; Score 13.6; DB 3; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20
DB 13 AGACTTCGCGAATTCACAT 32

RESULT 20
5221737-7
Patent No. 5221737
APPLICANT: BARTSCH, KLAUS;SCHULZ, ARNO;UHLMANN, EUGEN
TITLE OF INVENTION: GENE AND GENE STRUCTURE CODING FOR AN
AMINOTRANSFERASE, AND MICROORGANISMS WHICH EXPRESS THIS GENE
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//07/450,230
FILING DATE: 13-DEC-1989
SEQ ID NO: 7
LENGTH: 68
5221737-7

Query Match 64.8%; Score 13.6; DB 6; Length 68;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20
DB 4 AGATTACTAGGAATTCAAAT 23

RESULT 21
US-09-030-613-30
Sequence 30, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Florckiewicz, Robert Z.
APPLICANT: Baird, U. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue

```

; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,613
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083706tendburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.41BCL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-030-613-30

```

```

Query Match          63.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 CTAGGAATTCAATC 21
   |||||
Db 1 CTAGGAATTCAATC 15

```

```

RESULT 22
US-09-451-905-30
; Sequence 30, Application US/09451905
; Patent No. 6306613
; GENERAL INFORMATION:
; APPLICANT: Robert Z. Flokiewicz
; APPLICANT: Andrew Baird
; APPLICANT: Dale E. Warnock
; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
; TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME
; FILE REFERENCE: 200124.402C4
; CURRENT APPLICATION NUMBER: US/09/451,905
; CURRENT FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: Artificial Sequence
; OTHER INFORMATION: PCR Primer
;
US-09-451-905-30

```

```

Query Match          63.8%; Score 13.4; DB 4; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 CTAGGAATTCAATC 21
   |||||
Db 1 CTAGGAATTCAATC 15

```

```

RESULT 23
US-09-313-221A-77
; Sequence 77, Application US/09313221A
; Patent No. 6468743

```

```

; GENERAL INFORMATION:
; APPLICANT: Thomas L. Romick (Inventor)
; APPLICANT: Mark S. Fraser (Inventor)
; TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
; TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS
; FILE REFERENCE: HUNT-042784
; CURRENT APPLICATION NUMBER: US/09/313,221A
; CURRENT FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/086,025
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
;
US-09-313-221A-77

```

```

Query Match          63.8%; Score 13.4; DB 4; Length 40;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 7 CTAGGAATTCAATC 21
   |||||
Db 11 CTAGGAATTCAATC 25

```

```

RESULT 24
US-08-840-316-5/c
; Sequence 5, Application US/08840316
; Patent No. 6054567
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
; APPLICANT: Tsarev, Sergei, A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,316
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-840-316-5

```

Query Match 62.9%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 ATTTCTAGGAATCAAT 20
Db 20 ATGCTGTGGAATCAAT 3

RESULT 25
US-08-809-523-5/c
; Sequence 5, Application US/08809523
; Patent No. 6207416
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,523
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13102
; FILING DATE: 03-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/316,765
; FILING DATE: 03-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032US4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-809-523-5

; APPLICANT: Tsarev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,971
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/316,765
; FILING DATE: 03-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/947,263
; FILING DATE: 18-SEP-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-971-5

Query Match 62.9%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 ATTTCTAGGAATCAAT 20
Db 20 ATGCTGTGGAATCAAT 3

RESULT 27
US-09-402-776-5/c
; Sequence 5, Application US/09402776
; Patent No. 6458562
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
; APPLICANT: Tsarev, Sergei. A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,776
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/840,316
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-402-776-5

Query Match          62.9%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATTTCTAGGAATTCGAAT 20
DB 20 ATGCTGTGTAATTCGAAT 3

RESULT 28
PCT-US93-08849A-5/c
; Sequence 5, Application PC/US9308849A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08849A
; FILING DATE: 17-SEP-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William S. Feiler
; REGISTRATION NUMBER: 26,728
; REFERENCE/DOCKET NUMBER: 2026-4032 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
;
PCT-US93-08849A-5

Query Match          62.9%; Score 13.2; DB 5; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATTTCTAGGAATTCGAAT 20
DB 20 ATGCTGTGTAATTCGAAT 3

RESULT 29
PCT-US93-08849-5/c
; Sequence 5, Application PC/US9308849
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08849
; FILING DATE: 17-SEP-1993
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/947,263
; FILING DATE: 18-SEP-1992
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bork, Richard, W.
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
PCT-US93-08849-5

US-09-182-816-30/c
; Sequence 30, Application US/09182816
; Patent No. 6143542
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
```



```

; APPLICANT: Silver, Gary M.
; APPLICANT: Lo, Katherine C.
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
; FILE REFERENCE: FC-3-C1
; CURRENT APPLICATION NUMBER: US/09/182,816
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 08/989,510
; PRIOR FILING DATE: 1997-12-12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-182-816-30
```

```
Query Match      62.9%; Score 13.2; DB 3; Length 31;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 AGATTCTGAGATTCAA 18
        |||||
Db      19 AGATCTCTGAGATTCAA 2
```

```

RESULT 31
US-09-471-528-30/c
; Sequence 30, Application US/09471528
; Patent No. 6153397
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Silver, Gary M.
; APPLICANT: Lo, Katherine C.
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-3-C1-1
; CURRENT APPLICATION NUMBER: US/09/471,528
; CURRENT FILING DATE: 1999-12-27
; EARLIER APPLICATION NUMBER: 09/182,816
; EARLIER FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 08/989,510
; EARLIER FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-471-528-30
```

```
Query Match      62.9%; Score 13.2; DB 3; Length 31;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 AGATTCTGAGATTCAA 18
        |||||
Db      19 AGATCTCTGAGATTCAA 2
```

```

RESULT 32
US-09-634-530-30/c
; Sequence 30, Application US/09634530
; Patent No. 6290958
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
```

```

; APPLICANT: Silver, Gary M.
; APPLICANT: Lo, Katherine C.
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-3-C1-1
; CURRENT APPLICATION NUMBER: US/09/634,530
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 09/471,528
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 09/182,816
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 08/989,510
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-634-530-30
```

```
Query Match      62.9%; Score 13.2; DB 3; Length 31;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 AGATTCTGAGATTCAA 18
        |||||
Db      19 AGATCTCTGAGATTCAA 2
```

```

RESULT 33
US-07-955-041-6/c
; Sequence 6, Application US/07955041
; Patent No. 5360733
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, MINORU
; APPLICANT: BIERHUIZEN, MARTI FA
; TITLE OF INVENTION: A NOVEL BETAL-6
; TITLE OF INVENTION: N-ACETYLGLUCOSAMINYLTANSFERASE, ITS ACCEPTOR MOLECULE,
; TITLE OF INVENTION: LEUKOSIALIN AND A METHOD FOR CLONING PROTEINS HAVING
; TITLE OF INVENTION: ENZYMATIC ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,041
; FILING DATE: 19921001
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
```

TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-955-041-6

Query Match 62.9%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATTTCTAGCAATTCAAA 19
DB 18 GGTTTCTGCGAATTCAAA 1

RESULT 34
US-08-227-455-6/c
Sequence 6, Application US/08227455
Patent No. 5624832
GENERAL INFORMATION:
APPLICANT: FUKUDA, MINORU
APPLICANT: BIERHUIZEN, MARTI FA
TITLE OF INVENTION: A NOVEL BETAL-6
TITLE OF INVENTION: N-ACETYLGLUCOSAMINYLTRANSFERASE, ITS ACCEPTOR MOLECULE,
TITLE OF INVENTION: LEUCOSIALIN AND A METHOD FOR CLONING PROTEINS HAVING
TITLE OF INVENTION: ENZYMAITC ACTIVITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,455
FILING DATE: 14-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9957
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-227-455-6

Query Match 62.9%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATTTCTAGCAATTCAAA 19
DB 18 GGTTTCTGCGAATTCAAA 1

RESULT 35
US-08-472-482-6/c
Sequence 6, Application US/08472482
Patent No. 5638778
GENERAL INFORMATION:
APPLICANT: FUKUDA, MINORU
APPLICANT: BIERHUIZEN, MARTI FA

TITLE OF INVENTION: A NOVEL BETAL-6
TITLE OF INVENTION: N-ACETYLGLUCOSAMINYLTRANSFERASE, ITS ACCEPTOR MOLECULE,
TITLE OF INVENTION: LEUCOSIALIN AND A METHOD FOR CLONING PROTEINS HAVING
TITLE OF INVENTION: ENZYMAITC ACTIVITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

QY 2 GATTTCTAGCAATTCAAA 19
DB 18 GGTTTCTGCGAATTCAAA 1

RESULT 36
US-08-487-069-6/c
Sequence 6, Application US/08487069
Patent No. 5684134
GENERAL INFORMATION:
APPLICANT: FUKUDA, MINORU
APPLICANT: BIERHUIZEN, MARTI FA
TITLE OF INVENTION: A NOVEL BETAL-6
TITLE OF INVENTION: N-ACETYLGLUCOSAMINYLTRANSFERASE, ITS ACCEPTOR MOLECULE,
TITLE OF INVENTION: LEUCOSIALIN AND A METHOD FOR CLONING PROTEINS HAVING
TITLE OF INVENTION: ENZYMAITC ACTIVITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,069
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/955,041
FILING DATE: 01-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-487-069-6

Query Match 62.9%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATTCTAGGAATTCAA 19
DB 18 GGTTCGTGCGAATTCAA 1

RESULT 37
US-08-169-715-47/c
Sequence 47, Application US/08169715
Patent No. 6300056
GENERAL INFORMATION:
APPLICANT: Irvine, Bruce D.
APPLICANT: Horn, Thomas
APPLICANT: Chang, Chu-An
TITLE OF INVENTION: HIV PROBS FOR USE IN SOLUTION PHASE
TITLE OF INVENTION: SANDWICH HYBRIDIZATION ASSAYS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,715
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,583
FILING DATE: 18-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22300-20150.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-169-715-47

Query Match 62.9%; Score 13.2; DB 4; Length 33;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 20
DB 28 GCAATTCGGAAGTTCAT 9

RESULT 38
US-09-140-804-38
Sequence 38, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 63
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC15223
US-09-140-804-38

Query Match 62.9%; Score 13.2; DB 3; Length 63;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 46 AGAATCTAGGAATTCAT 63

RESULT 39
US-09-686-838B-38
Sequence 38, Application US/09686838B
Patent No. 6482612
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: Adipocyte-Specific Protein Homologs
FILE REFERENCE: 97-49D1
CURRENT APPLICATION NUMBER: US/09/686,838B
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/140,804
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: US 60/056,983
PRIOR FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 63
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC15223
US-09-686-838B-38

Query Match 62.9%; Score 13.2; DB 4; Length 63;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 12:00:17 ; Search time 126.318 Seconds
(without alignments)
448.773 Million cell updates/sec

Title: US-09-744-875a-1

Perfect score: 21
Sequence: 1 agattctcaggaattcaatc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2722628

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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5	18	85.7	21	ABT17265
6	18	85.7	63	ABT17327
7	18	85.7	100	AAA54479
8	18	85.7	100	AAA54480

9	18	85.7	100	ABA93801	KZ134 plasmid cons
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C	83	13.2	62.9	63	24	AAK24598	Linker primer ZC15
C	84	13.2	62.9	65	24	ABZ28545	Candida gene relat
C	85	13.2	62.9	72	16	AAAT01456	PCR primer GHVp79
C	86	13.2	62.9	78	24	ABSG68040	B-domain-deleted-F
C	87	13	61.9	20	24	ABNS58247	Related to Bombyx
C	88	13	61.9	21	17	AAAT32884	HTV-II gag p19 ge
C	89	13	61.9	21	20	AAAT29265	HTV-II gag p19 pr
C	90	13	61.9	22	25	ACA581182	Human familial b1p
C	91	13	61.9	23	25	ACA592226	Mouse phospholipid
C	92	13	61.9	26	16	AAAT04521	Human LBP (1-197) p
C	93	13	61.9	26	24	ABT04461	Human G-protein co
C	94	13	61.9	26	24	ABT04464	Human G-protein co
C	95	13	61.9	26	24	ABT04467	Human G-protein co
C	96	13	61.9	26	24	ABT04470	Human G-protein co
C	97	13	61.9	26	24	ABL92840	G protein-coupled
C	98	13	61.9	26	24	ABU92843	G protein-coupled
C	99	13	61.9	27	17	AAAT29257	C. difficile toxin
C	100	13	61.9	27	19	AAV30566	Clostridium diffic
C	101	13	61.9	33	24	ABSG7048	Human natriferic
C	102	13	61.9	35	17	AAAT12411	Soluble human eyr
C	103	13	61.9	40	17	AAAT33879	Human FKBP12 codin
C	104	13	61.9	50	21	AAAT5084	Oligonucleotide us
C	105	13	61.9	50	21	AAAD00190	Oligo BET-104 to g
C	106	13	61.9	50	24	ABZ02216	Human leukocyte ge
C	107	13	61.9	50	24	ABZ03732	Human leukocyte ge
C	108	13	61.9	51	25	ABZ77469	PCR primer for a t
C	109	13	61.9	65	24	ABNS8474	Mouse spliced tran
C	110	13	61.9	85	19	AAV21703	Thrombopoietin exp
C	111	13	61.9	85	19	AAV21704	Thrombopoietin exp
C	112	13	61.9	96	16	AAO80989	HIV protease inhib
C	113	13	61.9	96	16	AAO80986	HIV protease inhib
C	114	13	61.9	96	21	AACT2049	Human secreted pro
C	115	12.8	61.0	17	25	ABT38567	Tumour suppression
C	116	12.8	61.0	28	17	AAAT32202	Yeast cAMP-depende
C	117	12.8	61.0	30	15	AAO72219	Primer 3'C, amplif
C	118	12.8	61.0	30	16	AAAT11604	Human alpha-1C adr
C	119	12.8	61.0	30	22	AAAD16932	Staphylococcus aur
C	120	12.8	61.0	30	22	AAAG03316	Human PACE PCR pri
C	121	12.8	61.0	32	20	AAAX08584	Primer for humanis
C	122	12.8	61.0	33	24	AAAT19064	Human PCR primer h
C	123	12.8	61.0	34	21	AAAT43241	PCR primer for C.
C	124	12.8	61.0	36	21	AAAG56078	Rep fusion randoml
C	125	12.8	61.0	42	22	AAAT1834	C. perfringens end
C	126	12.8	61.0	43	17	AAAT30815	BGH transcription
C	127	12.8	61.0	43	18	AAAX59253	BGH transcription
C	128	12.8	61.0	43	19	AAAG60152	Reverse PCR primer
C	129	12.8	61.0	43	19	AAAT42392	Reverse PCR primer
C	130	12.8	61.0	43	20	AAAX58505	BGH transcription
C	131	12.8	61.0	43	20	AAAT70712	Reverse primer BGH
C	132	12.8	61.0	43	21	AAAT90801	Bovine growth horn
C	133	12.8	61.0	43	21	AAAT29298	Bovine growth horn
C	134	12.8	61.0	43	21	AAAT38808	Alphavirus related
C	135	12.8	61.0	43	24	ABK46274	Bovine growth horn
C	136	12.8	61.0	43	25	ABX81462	Bovine growth horn
C	137	12.8	61.0	50	24	ABZ04055	Human leukocyte ge
C	138	12.8	61.0	54	24	AAV49468	Signal sequence fo
C	139	12.8	61.0	60	24	ABNA3043	Human spliced tran
C	140	12.8	61.0	60	24	ABNA6682	Human spliced tran
C	141	12.8	61.0	61	21	AAAC69885	VEGF-binding nucle
C	142	12.8	61.0	61	21	AAAC69887	VEGF-binding nucle
C	143	12.8	61.0	65	24	ABZ27088	Candida essential
C	144	12.8	61.0	65	24	ABZ28178	Candida gene relat
C	145	12.8	61.0	65	24	ABN29091	Rat spliced transc
C	146	12.8	61.0	67	13	AAO36987	VIL, Ox VL 5'-end
C	147	12.8	61.0	83	22	AAAG23562	C. albicans essent
C	148	12.8	61.0	98	25	ABX20941	Human GDP-mannose
C	149	12.8	61.0	99	24	AAAG63130	Cell death protect
C	150	12.6	60.0	21	18	AAAT59533	Interleukin 2 rece
C	151	12.6	60.0	22	21	AAAT4872	Human apolipoprote
C	152	12.6	60.0	23	24	AAAD38675	Human CDKN1A gene
C	153	12.6	60.0	24	16	AAAT04845	PCR primer for ppr
C	154	12.6	60.0	24	24	ABO93709	Minimally cross-ly
C	155	12.6	60.0	27	16	AAO91224	Human Wnt primer-1
C	156	12.6	60.0	27	24	ABO82749	Human K-betam3 p27
C	157	12.6	60.0	27	24	ABV72205	PCR primer used to
C	158	12.6	60.0	30	16	AAO90503	Human beta-2 glyco
C	159	12.6	60.0	30	21	AAAO7855	Forward RH mapping
C	160	12.6	60.0	35	21	AAAG95970	PCR primer D used
C	161	12.6	60.0	35	21	AAAG95970	Human papillomavir
C	162	12.6	60.0	36	23	AAAT29642	Human HLA-DR alpha
C	163	12.6	60.0	37	24	ABT77138	Antisense primer f
C	164	12.6	60.0	39	24	ABSG1142	Human polymorphism
C	165	12.6	60.0	39	24	ABSG11276	Human polymorphism
C	166	12.6	60.0	48	20	AAAG5027	Human P selectin 1
C	167	12.6	60.0	51	22	AAAL27880	Human SNP oligonuc
C	168	12.6	60.0	51	22	AAAL30617	Human SNP oligonuc
C	169	12.6	60.0	51	22	AAAT76495	Human silent SNP c
C	170	12.6	60.0	60	24	ABN39177	Human spliced tran
C	171	12.6	60.0	60	24	ABN45757	Human spliced tran
C	172	12.6	60.0	60	24	ABN48071	Human spliced tran
C	173	12.6	60.0	60	24	ABN49731	Human spliced tran
C	174	12.6	60.0	60	24	ABNS50876	Candida essential
C	175	12.6	60.0	65	24	ABZ26625	Staphylococcus aur
C	176	12.6	60.0	70	18	AAV76443	Human thymopoiet
C	177	12.6	60.0	78	22	AAAT23682	Human brain expres
C	178	12.6	60.0	78	22	AAAT26908	Probe #16841 for g
C	179	12.6	60.0	78	22	AAAT5707	Probe #24393 used
C	180	12.6	60.0	80	23	ABSG49434	Human liver single
C	181	12.6	60.0	82	19	AAAT30402	PCR primer used to
C	182	12.6	60.0	82	19	AAV21701	Human thymopoiet
C	183	12.6	60.0	82	19	AAV21702	Human thymopoiet
C	184	12.6	60.0	93	16	AAAT19791	Human gene signatu
C	185	12.6	60.0	98	25	ABX33152	Human GDP-mannose
C	186	12.6	60.0	20	13	AAO31976	Synthetic oligomer
C	187	12.4	59.0	20	13	AAAG5635	Synthetic oligomer
C	188	12.4	59.0	20	13	AAAG5635	Human PARP-1 anti
C	189	12.4	59.0	21	21	AAAT76335	Human diallelic ma
C	190	12.4	59.0	26	20	AAAT5019	Cyclin-dependent K
C	191	12.4	59.0	26	20	AAAX0286	Clone t65 CDC2at
C	192	12.4	59.0	26	21	AAAG51420	Primer for A. thal
C	193	12.4	59.0	28	24	ABK13889	PCR primer TB-14 u
C	194	12.4	59.0	30	11	AAO04803	Phe-355 mutation o
C	195	12.4	59.0	30	17	AAAT34647	Primer for creatin
C	196	12.4	59.0	30	18	AAAT69804	Endo-beta-N-acetyl
C	197	12.4	59.0	30	21	AAAT75354	PCR primer BobBgr
C	198	12.4	59.0	31	20	AAAG3153	Treponema pallidum
C	199	12.4	59.0	36	20	AAAT07726	Pat-6 delta 9 desa
C	200	12.4	59.0	32	24	ABO73991	Phosphoenolpyruvat
C	201	12.4	59.0	33	24	ABAG5361	Human dihydrorota
C	202	12.4	59.0	34	20	AAAG1924	Porphorymonas ging
C	203	12.4	59.0	34	20	AAAG1924	Porphorymonas ging
C	204	12.4	59.0	37	24	ABL89405	C. boidinii DAS ge
C	205	12.4	59.0	40	21	AAAG59882	Babesia microti an
C	206	12.4	59.0	40	21	AAAG59882	Plasmodium falcipa
C	207	12.4	59.0	40	25	AAAG59882	Plasmodium Yoelli
C	208	12.4	59.0	40	25	AAAG59882	Primer #1 used in
C	209	12.4	59.0	41	19	AAAT7728	Maize polynormic
C	210	12.4	59.0	47	21	AAAG5975	Human mdp-related
C	211	12.4	59.0	50	22	AAAT76865	Human silent SNP c
C	212	12.4	59.0	50	22	AAAT76867	Human silent SNP c
C	213	12.4	59.0	50	24	ABZ02861	Human leukocyte ge
C	214	12.4	59.0	51	22	AAAT76864	Human silent SNP c
C	215	12.4	59.0	51	22	AAAT76866	Human silent SNP c
C	216	12.4	59.0	51	22	AAAT78102	Human silent SNP c
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C	218	12.4	59.0	65	24	ABNS2714	Mouse spliced tran
C	219	12.4	59.0	86	16	AAAT9798	Human gene signatu
C	220	12.2	58.1	17	19	AAV96668	Potato citrate syn
C	221	12.2	58.1	17	21	AAAF04361	Hammerhead ribozym
C	222	12.2	58.1	17	21	AAAF04809	Hammerhead ribozym
C	223	12.2	58.1	17	21	AAAF07457	Hammerhead ribozym
C	224	12.2	58.1	21	21	AAAT73972	Human biallelic ma
C	225	12.2	58.1	22	25	AAAG79335	Acetyl-Coenzyme A-
C	226	12.2	58.1	24	16	AAAT0849	Primer for amplif
C	227	12.2	58.1	24	16	AAAT0849	Cytomegalovirus pr

C 228	12.2	58.1	24	16	AA085703	Intronic primer fo	C 301	12	57.1	25	24	ABN13735	Human GDM/P-1 25-m
229	12.2	58.1	24	17	AA085703	Cucumber mosaic vi	C 302	12	57.1	25	24	ABN13736	Human GDM/P-1 25-m
230	12.2	58.1	24	21	AA085703	Primer amplifying	C 303	12	57.1	25	24	ABN13737	Human GDM/P-1 25-m
231	12.2	58.1	24	22	AA085703	Human PRO828 forwa	C 304	12	57.1	25	24	ABN13738	Human GDM/P-1 25-m
232	12.2	58.1	24	24	ABK28596	Human secreted or	C 305	12	57.1	25	24	ABN13739	Human GDM/P-1 25-m
233	12.2	58.1	24	25	ABX80248	Human secreted or	C 306	12	57.1	25	24	ABN13740	Human GDM/P-1 25-m
234	12.2	58.1	24	25	ABX80248	Human secreted or	C 307	12	57.1	25	24	ABN13740	Human GDM/P-1 25-m
235	12.2	58.1	24	25	ABX81135	Human secreted or	C 308	12	57.1	26	18	AA067064	Human GDM/P-1 25-m
236	12.2	58.1	24	25	ABX90225	Human secreted/tra	C 309	12	57.1	27	18	ABK67778	Soluble type I ins
237	12.2	58.1	24	25	ABX77836	Human secreted/tra	C 310	12	57.1	28	22	AA067348	Antibody cDNA PCR
238	12.2	58.1	24	25	ABX77836	Human PRO PCR prim	C 311	12	57.1	29	21	AA029209	D. melanogaster he
239	12.2	58.1	24	25	ABX77836	Human secreted/tra	C 312	12	57.1	29	21	AA029209	pH97 (+2) vector
240	12.2	58.1	24	25	ABX77836	Human PRO DNA PCR	C 313	12	57.1	29	21	AA029209	Primer H28 for det
C 241	12.2	58.1	26	21	AAZ93073	Human PRO PCR prim	C 314	12	57.1	29	21	AAZ93073	Granulocyte colony
242	12.2	58.1	28	21	AAZ93073	Primer used to gen	C 315	12	57.1	29	22	AA021738	Mouse SCR-1 cDNA a
C 243	12.2	58.1	29	21	AA077746	Human lysozyme I	C 316	12	57.1	29	22	AA021738	PCR primer #2 used
C 244	12.2	58.1	29	21	AA077746	Candida albicans a	C 317	12	57.1	30	16	AA096176	Interleukin-1beta
C 245	12.2	58.1	30	21	AA069971	VEGF-binding nucle	C 318	12	57.1	30	19	AAV54895	Primer 4 for human
C 246	12.2	58.1	30	22	AA069971	PCR primer used to	C 319	12	57.1	30	19	AAV54895	PCR primer used to
247	12.2	58.1	30	24	ABK67580	Novel Helicobacter	C 320	12	57.1	30	19	AAV54895	GST-XD4 primer 2.
248	12.2	58.1	30	24	ABK67580	Human SGR2-alpha 9	C 321	12	57.1	30	19	AAV54895	PCR primer used to
C 249	12.2	58.1	31	17	AA073322	Primer for amplify	C 322	12	57.1	30	20	AAV54895	Moraxella lactofer
C 250	12.2	58.1	31	20	AA080819	Plant lumaizine syn	C 323	12	57.1	30	21	AA073220	GST-XD4 (V323A)133
C 251	12.2	58.1	33	20	AA080819	BCOADC subunit B1	C 324	12	57.1	30	21	AA073220	Encephalomyocardit
C 252	12.2	58.1	33	24	ABK67580	Human leucine zipp	C 325	12	57.1	30	22	AA084680	PCR primer #6 used
C 253	12.2	58.1	33	24	ABK67580	Human B lymphocyte	C 326	12	57.1	30	22	AA084680	Encephalomyocardit
C 254	12.2	58.1	34	19	AAV33583	Pyrococcus horikos	C 327	12	57.1	30	24	ABK67580	Baobab microt an
C 255	12.2	58.1	34	22	AAH44207	Human SHC protein	C 328	12	57.1	30	24	AA024541	Encephalomyocardit
C 256	12.2	58.1	35	22	AAH77613	Human SHC kinase 35	C 329	12	57.1	31	20	AA062224	Mutagenic oligo #1
C 257	12.2	58.1	38	17	AA042470	Oligo M2 containin	C 330	12	57.1	31	21	AA062224	Human bi-allelic po
C 258	12.2	58.1	39	24	ABK67580	PCR primer KSE1.	C 331	12	57.1	31	21	AA062224	C. trachomatis pmp
C 259	12.2	58.1	40	19	AAV27005	Feline immunodef	C 332	12	57.1	31	22	AA062224	Oligo 9, used to a
C 260	12.2	58.1	46	16	AA086497	E2F-1 PCR primer.	C 333	12	57.1	31	22	AA062224	Human single nucle
C 261	12.2	58.1	47	20	AA086497	Human genome biall	C 334	12	57.1	31	22	AA062224	Chlamydia trachoma
C 262	12.2	58.1	51	22	AAH47665	Nucleotide sequenc	C 335	12	57.1	31	22	AA062224	SNP specific upper
C 263	12.2	58.1	51	24	ABK67580	SEF antibody and	C 336	12	57.1	31	24	ABK67580	Molecular antigen
C 264	12.2	58.1	52	21	AA086497	Human ovarian PCR-	C 337	12	57.1	31	24	ABK67580	Chlamydia DNA prim
C 265	12.2	58.1	53	21	AA086497	S. capricornis smal	C 338	12	57.1	31	24	ABK67580	Human growth hormo
C 266	12.2	58.1	53	21	AA086497	VEGF-binding nucle	C 339	12	57.1	32	17	AA086497	RT PCR primer for
C 267	12.2	58.1	58	21	AA070040	VEGF-binding nucle	C 340	12	57.1	32	21	AA086497	Primer for DNA seq
C 268	12.2	58.1	60	20	AA070040	Human LKB1 gene pr	C 341	12	57.1	33	21	AA086497	PCR primer used to
C 269	12.2	58.1	60	22	AA070040	Mouse LKB1 PCR pri	C 342	12	57.1	33	22	AA086497	C. parvum cryptopa
C 270	12.2	58.1	60	22	AA070040	Human LKB1 express	C 343	12	57.1	33	20	AA086497	Antisense PCR prim
C 271	12.2	58.1	60	22	AA070040	Human spliced tran	C 344	12	57.1	35	20	AA086497	Clostridium botuli
C 272	12.2	58.1	60	24	ABN37796	Human spliced tran	C 345	12	57.1	35	21	AA086497	PCR primer. Unde
C 273	12.2	58.1	60	24	ABN37796	MEK/ERK signal tra	C 346	12	57.1	35	24	ABK67580	Human protease act
C 274	12.2	58.1	61	21	AA069863	VEGF-binding nucle	C 347	12	57.1	35	24	ABK67580	PAR PCR primer SE0
C 275	12.2	58.1	64	22	AA069863	PCR primer for gly	C 348	12	57.1	36	18	AA069863	Human papillomavir
C 276	12.2	58.1	64	24	ABK67580	Pichia methanolica	C 349	12	57.1	36	22	AA069863	Primer BB1308 used
C 277	12.2	58.1	64	24	ABK67580	Human secreted pro	C 350	12	57.1	37	18	AA069863	Human HBG-7 recep
C 278	12.2	58.1	65	21	AA069863	CBE-tagged-Zs1g57	C 351	12	57.1	37	18	AA069863	Human IgG-2 heavy
C 279	12.2	58.1	65	21	AA069863	Candida essential	C 352	12	57.1	38	15	AA069863	Primer for amplifi
C 280	12.2	58.1	65	24	ABK67580	Candida gene relat	C 353	12	57.1	38	16	AA069863	Construction of pl
C 281	12.2	58.1	65	24	ABK67580	Mouse spliced tran	C 354	12	57.1	38	18	AA069863	PCR primer and pro
C 282	12.2	58.1	65	24	ABK67580	Upper PCR primer t	C 355	12	57.1	38	20	AA069863	Oligonucleotide us
C 283	12.2	58.1	65	24	ABK67580	Human cancer relat	C 356	12	57.1	38	24	ABK67580	Retroviral packagi
C 284	12.2	58.1	67	24	AA041830	Nucleotide sequenc	C 357	12	57.1	38	24	ABK67580	Primer used to amp
C 285	12.2	58.1	84	24	ABK67580	Candida albicans-s	C 358	12	57.1	38	25	AA069863	Human IgG2 Fc port
C 286	12.2	58.1	89	22	AAH42549	DNA binding protei	C 359	12	57.1	39	22	AA069863	Human monoclonal a
C 287	12.2	58.1	100	15	AA062584	BRCA1 mutation cor	C 360	12	57.1	39	22	AA069863	Endogenous human G
C 288	12.2	58.1	117	22	AA062584	Related to Bombyx	C 361	12	57.1	41	24	AA062584	Human G protein 44
C 289	12.2	58.1	122	20	AA062584	Oligonucleotide hy	C 362	12	57.1	41	24	AA062584	Oligonucleotide pr
C 290	12.2	58.1	122	20	AA062584	Rat beta-casein ST	C 363	12	57.1	41	24	AA062584	Oligonucleotide pr
C 291	12.2	58.1	122	21	AA062584	Human galectin-1 o	C 364	12	57.1	42	19	AA062584	PCR primer used to
C 292	12.2	58.1	122	21	AA062584	CMV gene fragmen	C 365	12	57.1	42	19	AA062584	PCR primer used to
C 293	12.2	58.1	122	22	AA062584	Nucleic acid of th	C 366	12	57.1	43	20	AA062584	Candida essential
C 294	12.2	58.1	122	22	AA062584	Nucleic acid of th	C 367	12	57.1	44	20	AA062584	RT-PCR primer #2 f
C 295	12.2	58.1	122	25	ABK67580	Isotopic purinore	C 368	12	57.1	47	21	AA062584	Human map-related

C 374	12	57.1	50	18	AA774745	EV152 used in cons	C 447	11.8	56.2	21	20	AAV65021	Human P selectin 1
C 375	12	57.1	50	21	AAZ43940	A. gossypii rib4 P	C 448	11.8	56.2	22	19	AAV67258	IFN-gamma PCR sens
C 376	12	57.1	50	24	ABZ00743	Human leukocyte ge	C 449	11.8	56.2	24	12	AAO10681	Probe for arginine
C 377	12	57.1	50	24	ABZ05089	Human leukocyte ge	C 450	11.8	56.2	24	17	AA741739	Clockwise primer f
C 378	12	57.1	50	24	ABZ05928	Human leukocyte ge	C 451	11.8	56.2	24	22	AAH31901	SNP specific primer f
C 379	12	57.1	50	24	ABZ07660	Human leukocyte ge	C 452	11.8	56.2	24	22	ABJ54213	Human CCR4 related
C 380	12	57.1	51	17	AA713495	Sept methylase 5'	C 453	11.8	56.2	25	15	AAO61498	Oligomer comprisin
C 381	12	57.1	51	22	AA559986	Canine IL-13Ralpha	C 454	11.8	56.2	25	19	AAV64592	Human native inter
C 382	12	57.1	51	22	AA766275	Human silent SNP c	C 455	11.8	56.2	25	19	AAV67060	Mouse ikaros oligo
C 383	12	57.1	51	22	AA769648	Human silent SNP c	C 456	11.8	56.2	25	21	AAV45353	Human Apob gene G
C 384	12	57.1	51	22	AA769648	Human silent SNP c	C 457	11.8	56.2	25	21	AAV45353	Human Apob gene G
C 385	12	57.1	52	20	AA575539	RT-PCR primer for	C 458	11.8	56.2	25	21	AAV45353	Human Apob gene G
C 386	12	57.1	52	20	AAH29538	Drosophila melanog	C 459	11.8	56.2	25	21	AAV45353	Human Apob gene G
C 387	12	57.1	53	21	AAA94948	S. neurena small r	C 460	11.8	56.2	27	22	AAH39258	SNP specific lower
C 388	12	57.1	53	21	AAA94948	T. gondii small r	C 461	11.8	56.2	27	22	AAH39258	Chicken fgt-4 gene
C 389	12	57.1	60	21	AA536674	Oligonucleotide us	C 462	11.8	56.2	28	22	AAH76130	Chicken fibroblast
C 390	12	57.1	60	21	AA536674	Oligonucleotide us	C 463	11.8	56.2	28	22	AAH76130	PCR primer for amp
C 391	12	57.1	60	21	AA536674	Oligonucleotide us	C 464	11.8	56.2	28	22	AAH76130	PCR primer for amp
C 392	12	57.1	60	24	ABN34077	Human spliced tran	C 465	11.8	56.2	28	24	ABJ41654	Chicken Pgf-4 gene
C 393	12	57.1	60	24	ABN34657	Human spliced tran	C 466	11.8	56.2	29	14	AAQ46190	pHPTSI sense prim
C 394	12	57.1	60	24	ABN35926	Human spliced tran	C 467	11.8	56.2	29	14	AAQ46190	GHI19-R3 reverse
C 395	12	57.1	60	24	ABN40968	Human spliced tran	C 468	11.8	56.2	29	21	AAV64604	Human native inter
C 396	12	57.1	60	24	ABN42010	Human spliced tran	C 469	11.8	56.2	29	21	AAV64604	Human Arp3H PCR pr
C 397	12	57.1	60	24	ABN44193	Human spliced tran	C 470	11.8	56.2	30	17	AAV70051	Chicken embryo let
C 398	12	57.1	60	24	ABN46845	Human spliced tran	C 471	11.8	56.2	30	21	AAV51328	Primer w258_ZMW14
C 399	12	57.1	60	24	ABN47723	Human spliced tran	C 472	11.8	56.2	30	21	AAV51328	Primer for Z. mays
C 400	12	57.1	60	24	ABN47723	Human spliced tran	C 473	11.8	56.2	30	21	AAV51328	Human G protein-co
C 401	12	57.1	60	25	AAV43383	G3 oligo (60mer) u	C 474	11.8	56.2	30	22	AAV55575	Staphylococcus aur
C 402	12	57.1	62	21	AAV47389	Oligonucleotide G3	C 475	11.8	56.2	32	20	AAV55575	Primer for Aquif cy
C 403	12	57.1	62	21	AAV47389	Chromosome 12 olig	C 476	11.8	56.2	32	22	AAH43950	Binary vector cons
C 404	12	57.1	65	21	AAZ92402	Human galectin-1 o	C 477	11.8	56.2	32	22	AAH43950	PCR primer used to
C 405	12	57.1	65	24	ABZ287573	Candida gene relat	C 478	11.8	56.2	32	16	AAH25186	Human apolipoprote
C 406	12	57.1	65	24	ABZ287573	Candida gene relat	C 479	11.8	56.2	33	21	AAH25186	Wildtype early reg
C 407	12	57.1	65	24	ABZ287573	Candida gene relat	C 480	11.8	56.2	33	21	AAH25186	Adenovirus 5 E2a r
C 408	12	57.1	65	24	ABZ287573	Rat spliced transc	C 481	11.8	56.2	33	22	AAH25186	PCR primer used to
C 409	12	57.1	65	24	ABZ287573	Rat spliced transc	C 482	11.8	56.2	33	22	AAH25186	Adenovirus E2a cod
C 410	12	57.1	65	24	ABZ287573	Mouse spliced tran	C 483	11.8	56.2	33	22	AAH25186	Adenovirus E2a pri
C 411	12	57.1	65	24	ABZ287573	Mouse spliced tran	C 484	11.8	56.2	33	22	AAH25186	PCR primer #2 for
C 412	12	57.1	65	24	ABZ287573	Mouse spliced tran	C 485	11.8	56.2	33	22	AAH25186	Transcription cont
C 413	12	57.1	78	24	ABX10528	BRCA1 exon1 mut G1	C 486	11.8	56.2	33	24	ABH55125	Human Myb protein
C 414	12	57.1	78	24	ABX10528	Human BRCA1 DNA fr	C 487	11.8	56.2	33	24	ABH55125	Human gamma glutam
C 415	12	57.1	84	21	AAV75363	Nucleotide fragmen	C 488	11.8	56.2	33	24	ABH55125	PCR primer specific
C 416	12	57.1	84	21	AAV75363	Human GDP-mannose	C 489	11.8	56.2	34	22	AAH45418	Human gamma globul
C 417	12	57.1	87	25	ABX10336	Human foetal liver	C 490	11.8	56.2	35	13	AAO28019	Primer for preCPB
C 418	12	57.1	87	22	AAK27235	Human brain expres	C 491	11.8	56.2	35	21	AAK28204	Primer 2265 for ma
C 419	12	57.1	88	22	AAK27235	Human bone marrow	C 492	11.8	56.2	35	21	AAK28204	Maize polymorphic
C 420	12	57.1	88	22	AAK27235	Human bone marrow	C 493	11.8	56.2	36	21	AAK28204	Human pancreatic c
C 421	12	57.1	89	22	AAK27235	Probe #23416 used	C 494	11.8	56.2	36	21	AAK28204	Human immune avidi
C 422	12	57.1	89	22	AAK27235	Human liver single	C 495	11.8	56.2	37	17	AAH37708	Human immune avidi
C 423	12	57.1	93	24	ABN71275	Streptococcus poly	C 496	11.8	56.2	41	17	AAH37708	Neisseria meningit
C 424	12	57.1	94	21	AAK17410	Human secreted pro	C 497	11.8	56.2	41	17	AAH37708	Oligonucleotide #2
C 425	12	57.1	95	21	AAK17410	Human secreted pro	C 498	11.8	56.2	41	19	AAH37708	Oligonucleotide #3
C 426	12	57.1	96	22	AAH57107	Probe #25793 used	C 499	11.8	56.2	41	19	AAH37708	PCR primer T2R5 us
C 427	12	57.1	96	22	AAH57107	N. gonorrhoeae nuc	C 500	11.8	56.2	41	24	ABZ57759	Human tissue inhib
C 428	12	57.1	97	16	AAO81929	Interferon-gamma b	C 501	11.8	56.2	41	24	ABZ57759	Forward PCR primer
C 429	12	57.1	97	21	AAH10062	"Mosaic" direct re	C 502	11.8	56.2	41	18	AAH10062	Human map-related
C 430	12	57.1	98	16	AAO81643	bEGF binding oligo	C 503	11.8	56.2	47	21	AAH10062	Human interferon-b
C 431	12	57.1	98	16	AAO81643	HIV protease inhib	C 504	11.8	56.2	47	21	AAH10062	Antisense primer u
C 432	12	57.1	98	16	AAO81643	HIV protease inhib	C 505	11.8	56.2	47	25	AAH10062	Human P selectin 1
C 433	12	57.1	98	22	AAH83310	Human ovarian PCR-	C 506	11.8	56.2	48	20	AAH10062	Probe used to isol
C 434	12	57.1	98	22	AAH83310	Human ovarian tumor	C 507	11.8	56.2	50	21	AAH10062	Human Apob gene A-
C 435	12	57.1	99	21	AAH83310	Human secreted pro	C 508	11.8	56.2	50	21	AAH10062	Human Apob gene A-
C 436	12	57.1	100	21	AAH83310	Human low adenosin	C 509	11.8	56.2	50	21	AAH10062	Human oligonucleot
C 437	12	57.1	100	21	AAH83310	Human adenosine re	C 510	11.8	56.2	50	21	AAH10062	Human oligonucleot
C 438	12	57.1	100	21	AAH83310	Human CD40 hammerh	C 511	11.8	56.2	50	21	AAH10062	Human PRO polytypic
C 439	12	57.1	100	21	AAH83310	Hammerhead ribozym	C 512	11.8	56.2	50	21	AAH10062	Human PRO221 Hybri
C 440	12	57.1	100	21	AAH83310	Hammerhead ribozym	C 513	11.8	56.2	50	21	AAH10062	
C 441	12	57.1	100	21	AAH83310	Human c-raf-1 onco	C 514	11.8	56.2	50	21	AAH10062	
C 442	12	57.1	100	21	AAH83310	Mass spectrometric	C 515	11.8	56.2	50	21	AAH10062	
C 443	12	57.1	100	21	AAH83310	Human RAD1 gene pr	C 516	11.8	56.2	50	21	AAH10062	
C 444	12	57.1	100	21	AAH83310	Recombinant HIV-1	C 517	11.8	56.2	50	21	AAH10062	
C 445	12	57.1	100	21	AAH83310	Zea mays root cap	C 518	11.8	56.2	50	21	AAH10062	
C 446	12	57.1	100	21	AAH83310	Helicobacter pylori	C 519	11.8	56.2	50	22	AAH10062	
C 447	12	57.1	100	21	AAH83310	Yeast detection pr	C 520	11.8	56.2	50	22	AAH10062	

C 520	11.8	56.2	50	24	ABZ00645	Human leukocyte ge	593	11.6	55.2	31	16	AAO93681	Human stromelysin
C 521	11.8	56.2	50	24	ABZ08100	Human leukocyte ge	594	11.6	55.2	31	16	AAQ93682	Human stromelysin
C 522	11.8	56.2	50	25	ACA54872	Novel secreted and	595	11.6	55.2	31	16	AAQ93791	Human stromelysin
C 523	11.8	56.2	50	25	ACA58357	Probe #14 used to	596	11.6	55.2	31	16	AAQ93792	Human stromelysin
C 524	11.8	56.2	50	25	ACA60064	Human secreted/tra	597	11.6	55.2	31	16	AAQ93793	Human stromelysin
C 525	11.8	56.2	50	25	ACA05402	Human secreted pro	598	11.6	55.2	31	16	AAQ93794	Human stromelysin
C 526	11.8	56.2	50	25	ABX96081	Human secreted/tra	599	11.6	55.2	31	17	AAK63698	Human stromelysin
C 527	11.8	56.2	50	25	ABX71512	Human secreted/tra	600	11.6	55.2	31	17	AAK63699	Human stromelysin
C 528	11.8	56.2	51	19	AAV07047	Truncated barbouri	601	11.6	55.2	31	17	AAK63700	Human stromelysin
C 529	11.8	56.2	51	19	AAV07042	Truncated barbouri	602	11.6	55.2	31	17	AAK63701	Human stromelysin
C 530	11.8	56.2	51	19	AAV06924	Truncated barbouri	603	11.6	55.2	31	17	AAK63587	Human stromelysin
C 531	11.8	56.2	51	22	AAI32091	Human SNP oligonuc	604	11.6	55.2	31	17	AAK63588	Human stromelysin
C 532	11.8	56.2	56	25	ABZ78486	Tumour suppression	605	11.6	55.2	31	17	AAK63589	Human stromelysin
C 533	11.8	56.2	56	25	ABZ09033	Human oligonucleot	606	11.6	55.2	32	15	AAQ68560	Primer for amplify
C 534	11.8	56.2	60	21	AAAI5063	5' PCR primer for	607	11.6	55.2	32	19	AAV23283	Nuclear location s
C 535	11.8	56.2	60	21	AAAD00167	Human interferon-b	608	11.6	55.2	33	22	AAH44347	Human DNA polymera
C 536	11.8	56.2	60	24	ABN31107	Human spliced tran	609	11.6	55.2	33	22	AAAF98246	C neofomans strai
C 537	11.8	56.2	60	24	ABN43173	Human spliced tran	610	11.6	55.2	33	24	ABQ83920	Mouse polycomb gen
C 538	11.8	56.2	60	24	ABN45708	Human spliced tran	611	11.6	55.2	33	24	ABD22242	Mouse polycomb gen
C 539	11.8	56.2	60	24	ABN45798	Human spliced tran	612	11.6	55.2	36	21	AAK32189	MVA 5' P13L flanki
C 540	11.8	56.2	62	21	AAZ96839	Human spliced tran	613	11.6	55.2	36	21	AAK32190	First probe subunit
C 541	11.8	56.2	64	16	AAQ87138	S. cerevisiae gene	614	11.6	55.2	36	21	AAA33202	Upstream target su
C 542	11.8	56.2	64	16	AAQ87138	Primer EV29 binds	615	11.6	55.2	36	21	AAA33219	Capture probe subu
C 543	11.8	56.2	64	17	AAAT32719	Oligo EV29 for cre	616	11.6	55.2	39	21	AAAT5930	PCR primer used to
C 544	11.8	56.2	64	18	AAAT60980	5'-end of alpha w	617	11.6	55.2	40	24	ABAS1672	Staphylococcus aur
C 545	11.8	56.2	64	19	AAV58337	Upstream primer EV	618	11.6	55.2	41	22	AAH44349	Human DNA polymera
C 546	11.8	56.2	64	22	AAAC81475	Primer EV29 for ha	619	11.6	55.2	41	24	ABQ83922	Mouse polycomb gen
C 547	11.8	56.2	65	21	AAAS58805	Human alpha globin	620	11.6	55.2	41	24	ABQ83923	Mouse polycomb gen
C 548	11.8	56.2	65	24	ABBS5154	Primer for the bet	621	11.6	55.2	42	22	AAI68554	Human cytochrome p
C 549	11.8	56.2	65	24	AAAD39790	Human galactosyltr	622	11.6	55.2	42	25	ABZ46263	PCR primer 24 used
C 550	11.8	56.2	65	24	ABN51792	ZC25564 PCR prim	623	11.6	55.2	42	25	ABZ24753	Human P-cadherin r
C 551	11.8	56.2	65	24	ABN56804	Mouse spliced tran	624	11.6	55.2	43	24	ABZ27765	Candida essential
C 552	11.8	56.2	65	24	ABN56804	Mouse spliced tran	625	11.6	55.2	44	22	ABD12978	Human DSP-13 cDNA
C 553	11.8	56.2	75	21	AAAC14517	Human secreted pro	626	11.6	55.2	45	10	AAAN91228	Linker sequence fo
C 554	11.8	56.2	91	21	AAAC19655	Human ovarian canc	627	11.6	55.2	46	16	AAO92024	polynucleotide use
C 555	11.8	56.2	92	21	ABX66053	Human secreted pro	628	11.6	55.2	46	20	AAZ23092	A. thaliana gene a
C 556	11.8	56.2	93	25	ABZ19317	Helicobacter pylor	629	11.6	55.2	47	21	AAZ67366	Human map-related
C 557	11.8	56.2	98	21	AAZ28944	Group III cDNA can	630	11.6	55.2	48	20	AAZ96657	Human cell antigen rec
C 558	11.8	56.2	98	21	AAZ42502	Human secreted pro	631	11.6	55.2	49	20	AAZ23769	Vector pAS1id PCR
C 559	11.8	56.2	100	22	AAAC83612	Human 5' EST isola	632	11.6	55.2	50	22	AAAL3800	Human SNP oligonuc
C 560	11.6	55.2	20	24	ABN79757	Saccharomyces cere	633	11.6	55.2	50	22	AAI75663	Human silent SNP c
C 561	11.6	55.2	22	22	AAAF24575	Human Fas target c	634	11.6	55.2	50	24	ABZ01004	Human leukocyte ge
C 562	11.6	55.2	22	22	ABT06693	PCR primer used fo	635	11.6	55.2	50	24	ABZ01075	Human leukocyte ge
C 563	11.6	55.2	22	24	ABX05519	Nucleic acid detec	636	11.6	55.2	50	24	ABZ02485	Human leukocyte ge
C 564	11.6	55.2	23	24	ABQ80686	PEPT B-3' adapter	637	11.6	55.2	50	24	ABZ02485	Human leukocyte ge
C 565	11.6	55.2	23	24	ABQ80686	Murine p85 PCR pri	638	11.6	55.2	51	22	AAI207859	Human leukocyte ge
C 566	11.6	55.2	24	24	ABQ93709	PCR primer for hum	639	11.6	55.2	51	22	AAI27324	Human SNP oligonuc
C 567	11.6	55.2	24	24	ABL53235	Minimally cross-hy	640	11.6	55.2	51	22	AAH39576	Human silent SNP c
C 568	11.6	55.2	24	24	ABL53235	PCR primer C-XBAI	641	11.6	55.2	51	22	AAH39576	Human SNP flankin
C 569	11.6	55.2	25	19	AAV62611	Ligase coenzyme A	642	11.6	55.2	52	16	AAI19845	Human SNP flankin
C 570	11.6	55.2	25	19	AAV22867	LO-CD2A chimeric a	643	11.6	55.2	52	16	AAI19845	Human gene signatu
C 571	11.6	55.2	25	19	AAV22867	MHC heavy chain ve	644	11.6	55.2	53	21	AAAS94949	S. muris small rib
C 572	11.6	55.2	25	20	AAZ10136	PCR primer used to	645	11.6	55.2	56	22	AAAF61490	Hirudin/oprf fusio
C 573	11.6	55.2	25	22	AAI69668	Hepatitis E virus	646	11.6	55.2	59	16	AAAT22863	Human gene signatu
C 574	11.6	55.2	25	22	AAH39675	SNP specific SNPE	647	11.6	55.2	60	20	AAH66432	Human single nucle
C 575	11.6	55.2	26	19	AAV62662	Humanised antibody	648	11.6	55.2	60	24	ABN34741	Human spliced tran
C 576	11.6	55.2	26	19	AAV22895	Humanised LO-CD2A	649	11.6	55.2	60	24	ABN36820	Human spliced tran
C 577	11.6	55.2	26	20	AAZ10195	PCR primer used to	650	11.6	55.2	60	24	ABN39541	Human spliced tran
C 578	11.6	55.2	27	24	ABX86266	Megaspinaera cerevi	651	11.6	55.2	60	24	ABN41514	Human spliced tran
C 579	11.6	55.2	27	25	ABLS5845	Human HPMRT gene hy	652	11.6	55.2	60	24	ABN44338	Human spliced tran
C 580	11.6	55.2	27	25	ABLS5845	Mouse HPMRT RT-PCR	653	11.6	55.2	60	24	ABN48166	Human spliced tran
C 581	11.6	55.2	28	22	AAAF24577	PCR primer used fo	654	11.6	55.2	60	24	ABN48166	Human spliced tran
C 582	11.6	55.2	28	24	ABD43093	T. pllicata TPDTR9g	655	11.6	55.2	64	13	AAQ25731	Human spliced tran
C 583	11.6	55.2	28	24	ABT06695	Nucleic acid detec	656	11.6	55.2	64	13	AAQ25731	N-terminal extrace
C 584	11.6	55.2	29	18	AAI96582	Primer OTG419 for	657	11.6	55.2	64	22	AAAF53414	PCR primer for gly
C 585	11.6	55.2	30	15	AAQ48421	Antisense primer f	658	11.6	55.2	64	24	ABK91350	Pichia methanolica
C 586	11.6	55.2	30	15	AAQ73169	Antisense primer f	659	11.6	55.2	64	24	AAK98884	Pichia methanolica
C 587	11.6	55.2	30	16	AAAT93942	Primer 75 for huma	660	11.6	55.2	65	22	AAA14522	PCR primer used to
C 588	11.6	55.2	30	16	AAAT93942	Antisense primer 7	661	11.6	55.2	65	22	AAAD18424	Ashbya gossypii ge
C 589	11.6	55.2	30	19	AAV34557	Antisense primer 7	662	11.6	55.2	65	24	ABZ26436	Candida gene relat
C 590	11.6	55.2	30	19	AAV34557	Human sapiens RNA 3	663	11.6	55.2	65	24	ABZ28550	Candida gene relat
C 591	11.6	55.2	30	20	AAAX87928	Human PCIP PCR pri	664	11.6	55.2	65	24	ABZ28778	Candida gene relat
C 592	11.6	55.2	31	16	AAAX21759	ApOB promoter BCB	665	11.6	55.2	65	24	ABZ28935	Candida gene relat
C 593	11.6	55.2	31	16	AAQ93680	Human stromelysin	666	11.6	55.2	65	24	ABN28846	Rat spliced transc

666	11.6	55.2	65	24	ABN30342	Rat spliced transc	c 739	11.4	54.3	20	21	AAA41115	Human TNFalpha ant
667	11.6	55.2	65	24	ABN53729	Mouse spliced tran	740	11.4	54.3	20	21	AAZ89825	PCR primer for car
668	11.6	55.2	65	24	ABN55272	Mouse spliced tran	741	11.4	54.3	20	21	AAZ88018	Human umbilical ve
669	11.6	55.2	66	20	ABH85630	Human single nucle	742	11.4	54.3	21	21	AAA97254	PRRV attenuated v
670	11.6	55.2	68	24	ABJ36201	C. elegans connect	c 743	11.4	54.3	21	21	ABK27416	Human papillomavir
671	11.6	55.2	69	24	ABJ98840	Oligonucleotide MP	744	11.4	54.3	21	25	ABZ23539	PCR primer used to
672	11.6	55.2	72	19	AAV62650	Humanised antibody	745	11.4	54.3	21	25	ABZ23555	PCR primer used to
673	11.6	55.2	72	20	AAZ32795	Reshaped F19 light	746	11.4	54.3	21	19	AAV70499	Leistad virus pri
674	11.6	55.2	72	20	AAZ32800	Reshaped F19 light	c 747	11.4	54.3	23	20	AAZ30818	STAR-3 specific ol
675	11.6	55.2	72	20	AAZ10183	Oligonucleotide 12	c 748	11.4	54.3	23	22	AAZ3446	Reverse PCR primer
676	11.6	55.2	72	21	AACT1559	Human secreted pro	749	11.4	54.3	24	24	ABJ54091	Human nucleotide e
677	11.6	55.2	72	21	AACT1534	Human secreted pro	c 750	11.4	54.3	24	24	ABJ54091	Human zinc finger
678	11.6	55.2	74	20	AAV72480	D. pterocynissus D	c 751	11.4	54.3	24	25	AAJ53759	Single sequence 1e
679	11.6	55.2	75	20	AAJ37817	Primer 2. Synthet	c 752	11.4	54.3	25	16	AAQ81978	Human soluble lamp
680	11.6	55.2	75	22	ABX19763	Human brain expres	c 753	11.4	54.3	25	19	AAQ09946	Human CDP-diacylg
681	11.6	55.2	75	23	ABJ54574	Human liver single	c 754	11.4	54.3	25	24	ABK69046	Human alpha relate
682	11.6	55.2	75	24	ABJ54063	Human genome-deriv	c 755	11.4	54.3	25	25	ABK95049	Human oligonucleot
683	11.6	55.2	76	19	AAV21712	Thrombopoietin exp	c 756	11.4	54.3	25	25	ABX10925	Human CDP-diacylg
684	11.6	55.2	77	7	AAV60749	Sequence encoding	c 757	11.4	54.3	26	14	AAQ40023	PCR primer for OTC
685	11.6	55.2	77	19	AAV60750	Sequence encoding	c 758	11.4	54.3	26	15	AAV45540	Human OTC gene pri
686	11.6	55.2	77	19	AAV11545	Human biallelic po	c 759	11.4	54.3	26	15	AAV45540	Helicobacter pylor
687	11.6	55.2	78	18	AAV79205	Staphylococcus aur	c 760	11.4	54.3	27	15	AAQ61018	COL2A1 3'-primer (
688	11.6	55.2	78	25	AAV52080	Anti-ovarian cance	761	11.4	54.3	27	16	AAQ91225	Human Wnt primer-2
689	11.6	55.2	79	22	ABJ48892	Human breast cell	762	11.4	54.3	27	17	AAV72010	Primer detects mar
690	11.6	55.2	79	22	ABJ49393	Human breast cell	763	11.4	54.3	27	17	AAV71938	Primer detects mar
691	11.6	55.2	79	22	ABJ67303	Human foetal liver	c 764	11.4	54.3	27	21	AAA61722	Human serine prote
692	11.6	55.2	79	22	ABJ3875	Probe #12341 for g	c 765	11.4	54.3	27	22	AAH75625	Aminoglycoside 3'-
693	11.6	55.2	79	22	ABJ34397	Probe #12863 for g	c 766	11.4	54.3	27	23	ABJ53329	Artificial secreto
694	11.6	55.2	79	22	AAK15740	Human brain expres	c 767	11.4	54.3	27	23	ABJ53329	Primer STAS for h
695	11.6	55.2	79	22	AAK10965	Human bone marrow	c 768	11.4	54.3	29	17	AAJ33710	Primer FAT2 used
696	11.6	55.2	79	22	AAK14177	Human bone marrow	c 769	11.4	54.3	29	22	AAH38245	SNP specific upper
697	11.6	55.2	79	22	AAK12735	Probe #11668 for g	c 770	11.4	54.3	29	22	AAH38245	Human TAC1-Fc fusi
698	11.6	55.2	79	22	AAI22225	Probe #12158 for g	771	11.4	54.3	30	25	AAJ53763	M3mp18 PCR primer
699	11.6	55.2	79	22	AAI47020	Probe #15706 used	c 772	11.4	54.3	30	21	AAJ58275	Nucleotide sequenc
700	11.6	55.2	79	22	AAI47520	Probe #16206 used	c 773	11.4	54.3	30	21	ABJ41542	Forward PCR primer
701	11.6	55.2	79	22	AAI07420	Probe #7914 used t	774	11.4	54.3	30	22	AAJ50697	Forward PCR primer
702	11.6	55.2	79	23	AAI07923	Human liver single	775	11.4	54.3	30	22	AAJ50691	Forward PCR primer
703	11.6	55.2	79	23	ABJ40548	Human liver single	776	11.4	54.3	30	22	AAJ50691	Forward PCR primer
704	11.6	55.2	79	23	ABJ41068	Human liver single	c 777	11.4	54.3	30	24	ABQ84680	Paddy rice meiotic
705	11.6	55.2	79	24	ABJ41932	Human genome-deriv	c 778	11.4	54.3	31	19	AAV03561	Probe b10a for re
706	11.6	55.2	79	24	ABJ51542	Human genome-deriv	c 779	11.4	54.3	31	20	AAJ17797	Wheat oxalate oxid
707	11.6	55.2	82	19	AAV21714	Thrombopoietin exp	780	11.4	54.3	31	20	AAJ02833	Wheat oxalate oxid
708	11.6	55.2	82	19	AAV21714	Thrombopoietin exp	c 781	11.4	54.3	32	16	AAQ83193	Primer used to cre
709	11.6	55.2	82	22	AAK24845	Probe #19197 for g	c 782	11.4	54.3	33	22	AAH75925	Human ATPase 30 c
710	11.6	55.2	82	22	AAK24845	Human brain expres	c 783	11.4	54.3	33	22	AAH75925	Mutant human facto
711	11.6	55.2	82	22	AAK24845	Human bone marrow	c 784	11.4	54.3	33	22	AAJ51737	Heparin binding pr
712	11.6	55.2	86	21	AAK24845	Human genome-deriv	c 785	11.4	54.3	33	24	ABJ56688	Fragile intelligen
713	11.6	55.2	90	22	AAK24845	Tetracycline promo	c 786	11.4	54.3	33	24	ABJ56688	Human phosphatid
714	11.6	55.2	91	24	ABQ94467	Tumour suppression	c 787	11.4	54.3	33	24	ABJ56688	Human serine thre
715	11.6	55.2	95	21	AAK26011	Human secreted pro	c 788	11.4	54.3	34	20	AAJ91970	Porphyromonas ging
716	11.6	55.2	97	16	AAO80978	HIV protease inhib	c 789	11.4	54.3	34	25	ABT73365	Endothelially expr
717	11.6	55.2	97	16	AAO80978	HIV protease inhib	c 790	11.4	54.3	35	24	ABK47845	Borrelia OspA-B31/
718	11.6	55.2	97	16	AAO80978	HIV protease inhib	c 791	11.4	54.3	36	16	AAO80978	Alur gene PCR pri
719	11.6	55.2	97	21	AAJ41054	Human low adenosin	c 792	11.4	54.3	36	19	AAV59183	Human bak BH2 doma
720	11.6	55.2	98	16	AAJ41054	Human adenosine re	c 793	11.4	54.3	36	19	AAV59183	Cryptococcus nodae
721	11.6	55.2	98	16	AAQ80986	Interferon-gamma b	c 794	11.4	54.3	37	19	AAV62623	LO-CD2a chimeric a
722	11.6	55.2	98	16	AAQ80986	HIV protease inhib	c 795	11.4	54.3	37	20	AAJ210148	PCR primer used to
723	11.6	55.2	98	16	AAQ80986	HIV protease inhib	c 796	11.4	54.3	38	24	ABK47847	Borrelia OspA-B31/
724	11.6	55.2	99	25	ABK06081	Tumour suppression	c 797	11.4	54.3	38	24	ABK47847	Apal restriction s
725	11.6	55.2	100	21	AAK13251	S. pneumoniae type	c 798	11.4	54.3	38	24	ABK47847	Apal restriction s
726	11.6	55.2	100	21	AAK13251	Human secreted pro	799	11.4	54.3	39	16	AAJ03007	CryI toxin PCR pri
727	11.4	54.3	13	23	ABJ18840	Bovine beta-casein	800	11.4	54.3	39	16	AAJ03007	Primer A for CryI
728	11.4	54.3	13	23	ABJ18840	Oligonucleotide SE	801	11.4	54.3	39	16	AAJ03007	Bt toxin PCR prime
729	11.4	54.3	15	17	AAK65579	Oligonucleotide SE	802	11.4	54.3	39	19	AAV26116	SIV NA gene PCR pr
730	11.4	54.3	15	17	AAK65579	Human CD40 hammet	803	11.4	54.3	39	21	AAZ58029	Swine influenza vi
731	11.4	54.3	17	13	AAQ23301	Probe to alphaF-P	804	11.4	54.3	39	22	AAH23891	E coli ATP synthas
732	11.4	54.3	18	22	AAK21745	Competitor oligo A	805	11.4	54.3	39	22	AAH23891	E coli ATP synthas
733	11.4	54.3	20	20	AAK26521	Human SRC-3 antise	806	11.4	54.3	41	22	AAH78578	Upstream primer MP
734	11.4	54.3	20	20	AAK26521	Primer used to amp	c 807	11.4	54.3	41	22	AAK26521	Mutant human facto
735	11.4	54.3	20	20	AAK26521	E. coli SecA antise	c 808	11.4	54.3	42	22	AAH78578	Human GHRH 9.13 pr
736	11.4	54.3	20	20	AAK26521	Reverse primer for	c 809	11.4	54.3	42	22	AAH78578	C parvum Col5/60 p
737	11.4	54.3	20	21	AAH86113	Human rchd024 gene	810	11.4	54.3	43	24	ABK67860	Mouse MHC S1YK enc
738	11.4	54.3	20	21	AAH86113	Human TNFalpha ant	c 811	11.4	54.3	43	24	ABK67860	Candida essential

C 812	11.4	54.3	44	16	AAT04749	PCR primer, EPs42K	C 885	11.4	54.3	64	21	AA011152	Human secreted pro
C 813	11.4	54.3	45	20	AAZ31029	PCR primer #3 used	C 886	11.4	54.3	65	24	ABZ26239	Candida essential
C 814	11.4	54.3	45	22	AAFS4768	PCR primer used to	C 887	11.4	54.3	65	24	ABZ28505	Candida gene relat
C 815	11.4	54.3	45	24	ABQ81581	Luciferase gene mu	C 888	11.4	54.3	65	24	ABZ29627	Candida gene relat
C 816	11.4	54.3	45	24	ABQ81582	Luciferase gene mu	C 889	11.4	54.3	65	24	ABN31044	Rat spliced trans
C 817	11.4	54.3	47	21	AAZ92750	Escherichia coli a	C 890	11.4	54.3	65	24	ABN54270	Mouse spliced tran
C 818	11.4	54.3	47	21	ABL54032	Aldehyde dehydroge	C 891	11.4	54.3	65	24	ABN55263	Mouse spliced tran
C 819	11.4	54.3	49	19	ABV64234	Plasmid pGL2-SMA2p	C 892	11.4	54.3	66	16	AAT04742	PCR primer, P1B, u
C 820	11.4	54.3	49	25	ABZ25329	PCR primer MFK150,	C 893	11.4	54.3	67	15	AA068767	Almond HMUS PCR pr
C 821	11.4	54.3	50	20	AAZ34323	Human PRO298 hybr	C 894	11.4	54.3	67	15	AAQ63670	TMF-alpha ribozyme
C 822	11.4	54.3	50	21	AACT8900	Human PRO298 hybr	C 895	11.4	54.3	67	16	AAT24754	Human gene signatu
C 823	11.4	54.3	50	21	AAA28194	Target molecule us	C 896	11.4	54.3	67	18	AAT45405	Specific ribozyme
C 824	11.4	54.3	50	21	AAA28197	Detection probe us	C 897	11.4	54.3	67	20	AA058876	Interleukin 2 ribo
C 825	11.4	54.3	50	22	AAI77541	Human silent SNP c	C 898	11.4	54.3	68	25	ABZ78194	Tumour suppression
C 826	11.4	54.3	50	22	ABZ00506	Human leukocyte ge	C 899	11.4	54.3	68	25	ABZ09741	Human oligonucleot
C 827	11.4	54.3	50	24	ABZ00962	Human leukocyte ge	C 900	11.4	54.3	69	17	AAT34308	Human CASBPORI fo
C 828	11.4	54.3	50	24	ABZ02058	Human leukocyte ge	C 901	11.4	54.3	70	15	AAQ19273	Primer B850 to amp
C 829	11.4	54.3	50	24	ABZ02257	Human leukocyte ge	C 902	11.4	54.3	70	25	ABZ78951	Tumour suppression
C 830	11.4	54.3	50	24	ABZ03782	Human leukocyte ge	C 903	11.4	54.3	70	25	ABZ09498	Human oligonucleot
C 831	11.4	54.3	50	24	ABZ03923	Human leukocyte ge	C 904	11.4	54.3	71	24	ABL57259	T4 ipIII gene tran
C 832	11.4	54.3	50	24	ABZ04069	Human leukocyte ge	C 905	11.4	54.3	71	24	AAQ76253	Protease (I-247)/CK
C 833	11.4	54.3	50	24	ABZ04291	Human leukocyte ge	C 906	11.4	54.3	75	19	AAV69222	Wild type coding s
C 834	11.4	54.3	50	24	ABZ04480	Human leukocyte ge	C 907	11.4	54.3	78	24	ABN63108	Human cancer relat
C 835	11.4	54.3	50	24	ABZ05699	Human leukocyte ge	C 908	11.4	54.3	81	14	AAQ49564	Bet Cyst Nematode
C 836	11.4	54.3	50	24	AAI41463	MSMAP-5'-T7 linker	C 909	11.4	54.3	81	16	AAT06225	HIV-1 reverse tran
C 837	11.4	54.3	50	25	ABX92695	Human PRO DNA prob	C 910	11.4	54.3	85	22	AAK60150	Human immune/haema
C 838	11.4	54.3	50	25	ABZ85170	Toxicologically re	C 911	11.4	54.3	85	24	ABL75879	Corn tassell-derive
C 839	11.4	54.3	51	22	AAI27032	Human SNP oligonuc	C 912	11.4	54.3	86	19	AAV59503	Upstream primer fo
C 840	11.4	54.3	51	22	AAI32187	Human SNP oligonuc	C 913	11.4	54.3	86	19	AAV34146	Upstream primer fo
C 841	11.4	54.3	51	22	AAI73406	Human silent SNP c	C 914	11.4	54.3	86	19	AAV34278	Upstream primer fo
C 842	11.4	54.3	51	22	AAI73407	Human silent SNP c	C 915	11.4	54.3	86	19	AAV69603	Upstream primer fo
C 843	11.4	54.3	51	22	AAI75979	Human silent SNP c	C 916	11.4	54.3	86	20	AAZ32073	Gamma activation s
C 844	11.4	54.3	51	22	AAI76855	Human silent SNP c	C 917	11.4	54.3	86	20	AAZ19852	SV40 early promote
C 845	11.4	54.3	51	22	AAI77358	Human silent SNP c	C 918	11.4	54.3	86	20	AAZ24803	Upstream primer fo
C 846	11.4	54.3	51	22	AAI77359	Human silent SNP c	C 919	11.4	54.3	86	20	AAZ09776	Synthetic GAS-cont
C 847	11.4	54.3	51	22	AAI78103	Human silent SNP c	C 920	11.4	54.3	86	20	AAZ10678	PCR primer used to
C 848	11.4	54.3	51	23	ABL00202	Human silent nonco	C 921	11.4	54.3	86	20	AAZ00402	Human GAS promoter
C 849	11.4	54.3	52	12	AAQ10819	Mutated section of	C 922	11.4	54.3	86	20	AAZ00794	SV40 early promote
C 850	11.4	54.3	52	14	AAQ38444	pTPO(M1)-BS mutat	C 923	11.4	54.3	86	20	AAZ06211	Upstream primer fo
C 851	11.4	54.3	52	14	AAQ40070	Human TPO gene seq	C 924	11.4	54.3	86	20	AAZ97908	Upstream primer fo
C 852	11.4	54.3	52	20	AAZ24338	Oligonucleotide 01	C 925	11.4	54.3	86	20	AAZ19003	Upstream primer fo
C 853	11.4	54.3	52	24	AAI41462	MSMAP-5'-T7 linker	C 926	11.4	54.3	86	20	AAZ8669	Nucleotide sequenc
C 854	11.4	54.3	54	18	AAT98091	N-terminal primer	C 927	11.4	54.3	86	20	AAZ84925	Upstream primer fo
C 855	11.4	54.3	54	20	AAI19882	ED7-HIV p17/p24 ge	C 928	11.4	54.3	86	20	AAZ35893	PCR primer used to
C 856	11.4	54.3	54	20	AAI19526	ED7-HIV p17/p24 ge	C 929	11.4	54.3	86	20	AAZ37361	Human GAS-containi
C 857	11.4	54.3	55	21	AAAC11245	Human secreted pro	C 930	11.4	54.3	86	20	AAZ37443	Synthetic GAS-cont
C 858	11.4	54.3	57	16	AAT05761	Thermophilic stran	C 931	11.4	54.3	86	20	AAZ27303	Upstream primer fo
C 859	11.4	54.3	57	22	AAD03427	MSV GC-rich elemen	C 932	11.4	54.3	86	20	AAZ51693	5' PCR primer used
C 860	11.4	54.3	57	24	ABL57260	T4 gene ipIII tran	C 933	11.4	54.3	86	20	AAZ30175	Upstream primer fo
C 861	11.4	54.3	57	24	ABL57261	Staphylococcus aur	C 934	11.4	54.3	86	20	AAZ22203	Upstream primer fo
C 862	11.4	54.3	58	18	AAV76131	Human secreted pro	C 935	11.4	54.3	86	20	AAZ22103	Upstream primer fo
C 863	11.4	54.3	59	21	AAAC29473	Human secreted pro	C 936	11.4	54.3	86	20	AAZ30309	5' PCR primer used
C 864	11.4	54.3	60	24	ABN32567	Human spliced tran	C 937	11.4	54.3	86	20	AAZ20404	Upstream primer fo
C 865	11.4	54.3	60	24	ABN334745	Human spliced tran	C 938	11.4	54.3	86	20	AAZ16170	SV40 early promote
C 866	11.4	54.3	60	24	ABN37978	Human spliced tran	C 939	11.4	54.3	86	20	AAZ04303	Upstream primer fo
C 867	11.4	54.3	60	24	ABN38082	Human spliced tran	C 940	11.4	54.3	86	20	AAZ00603	Upstream primer fo
C 868	11.4	54.3	60	24	ABN38346	Human spliced tran	C 941	11.4	54.3	86	20	AAV08847	Primer for DNA enc
C 869	11.4	54.3	60	24	ABN39207	Human spliced tran	C 942	11.4	54.3	86	21	AAV84403	Upstream primer fo
C 870	11.4	54.3	60	24	ABN42543	Human spliced tran	C 943	11.4	54.3	86	21	AAD02079	SV40 promoter sequ
C 871	11.4	54.3	60	24	ABN43967	Human spliced tran	C 944	11.4	54.3	86	21	AAD02231	5' PCR primer to g
C 872	11.4	54.3	60	24	ABN44010	Human spliced tran	C 945	11.4	54.3	86	21	AAZ22033	Upstream PCR prime
C 873	11.4	54.3	60	24	ABN44587	Human spliced tran	C 946	11.4	54.3	86	21	AAZ22308	Upstream primer fo
C 874	11.4	54.3	60	24	ABN46719	Human spliced tran	C 947	11.4	54.3	86	21	AAZ22365	Upstream primer fo
C 875	11.4	54.3	60	24	ABN49966	Human spliced tran	C 948	11.4	54.3	86	21	AAZ98765	Upstream primer fo
C 876	11.4	54.3	60	24	ABN50295	Human spliced tran	C 949	11.4	54.3	86	21	AAAC99233	Upstream primer fo
C 877	11.4	54.3	60	24	ABN58991	Human spliced tran	C 950	11.4	54.3	86	21	AAAC99810	Upstream primer fo
C 878	11.4	54.3	60	24	ABN59113	Human spliced tran	C 951	11.4	54.3	86	21	AAAF16507	Upstream primer fo
C 879	11.4	54.3	60	24	ABN59320	Human spliced tran	C 952	11.4	54.3	86	21	AAAF18426	Upstream PCR prime
C 880	11.4	54.3	61	19	AAV07498	Leiyshad virus prt	C 953	11.4	54.3	86	21	AAAF66217	Upstream primer fo
C 881	11.4	54.3	61	21	AAAF97255	PRRSV attenuated v	C 954	11.4	54.3	86	21	AAAC66402	GAS reporter const
C 882	11.4	54.3	61	24	AAAD24033	PRRSV recombinant	C 955	11.4	54.3	86	21	AAAC67623	Upstream primer fo
C 883	11.4	54.3	61	25	ABZ23556	PCR primer used to	C 956	11.4	54.3	86	21	AAAC8073	Upstream primer fo
C 884	11.4	54.3	63	21	AAAC30615	Human secreted pro	C 957	11.4	54.3	86	21	AAAC81702	GAS reporter const

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c 958 11.4 54.3 86 21 AAC93302 Upstream primer fo
c 959 11.4 54.3 86 21 AAC93356 Upstream primer fo
c 960 11.4 54.3 86 21 AAC93414 Upstream primer fo
c 961 11.4 54.3 86 21 AAC93471 Upstream primer fo
c 962 11.4 54.3 86 21 AAC95454 Upstream primer fo
c 963 11.4 54.3 86 21 AAC95513 Upstream primer fo
c 964 11.4 54.3 86 21 AAC96892 SV40 promoter upst
c 965 11.4 54.3 86 21 AAA98975 SV40 early promote
c 966 11.4 54.3 86 21 AAA98984 SV40 early promote
c 967 11.4 54.3 86 21 AAA98993 SV40 early promote
c 968 11.4 54.3 86 21 AAC98982 GAS reporter const
c 969 11.4 54.3 86 21 AAC99041 GAS reporter const
c 970 11.4 54.3 86 21 AAC99100 GAS reporter const
c 971 11.4 54.3 86 21 AAC99269 SV40 promoter upst
c 972 11.4 54.3 86 21 AAC99327 SV40 promoter upst
c 973 11.4 54.3 86 21 AAC99384 SV40 promoter upst
c 974 11.4 54.3 86 21 AAC99499 Upstream primer fo
c 975 11.4 54.3 86 21 AAC99616 Upstream primer fo
c 976 11.4 54.3 86 21 AAC99671 SV40 promoter upst
c 977 11.4 54.3 86 21 AAC93402 GAS reporter const
c 978 11.4 54.3 86 21 AAC74215 Upstream primer fo
c 979 11.4 54.3 86 21 AAC74272 Upstream primer fo
c 980 11.4 54.3 86 21 AAC74329 Upstream primer fo
c 981 11.4 54.3 86 21 AAC74388 Upstream primer fo
c 982 11.4 54.3 86 21 AAC78450 Upstream primer fo
c 983 11.4 54.3 86 21 AAC78989 Upstream primer fo
c 984 11.4 54.3 86 21 AAC79673 Upstream primer fo
c 985 11.4 54.3 86 21 AAC79732 Upstream primer fo
c 986 11.4 54.3 86 21 AAC79791 Upstream primer fo
c 987 11.4 54.3 86 21 AAC80523 Upstream primer fo
c 988 11.4 54.3 86 21 AAC81020 Upstream primer fo
c 989 11.4 54.3 86 21 AAC81078 Upstream primer fo
c 990 11.4 54.3 86 21 AAA95093 Upstream primer fo
c 991 11.4 54.3 86 21 AAC99207 Upstream primer fo
c 992 11.4 54.3 86 21 AAC99441 Upstream primer fo
c 993 11.4 54.3 86 21 AAC99558 Upstream primer fo
c 994 11.4 54.3 86 21 AAC99730 Upstream primer fo
c 995 11.4 54.3 86 21 AAC99899 Upstream primer fo
c 996 11.4 54.3 86 21 AAC99958 Upstream primer fo
c 997 11.4 54.3 86 21 AAC60017 Upstream primer fo
c 998 11.4 54.3 86 21 AAC69076 Upstream primer fo
c 999 11.4 54.3 86 21 AAC69391 Upstream primer fo
c1000 11.4 54.3 86 21 AAC69447 Upstream primer fo

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ALIGNMENTS

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RESULT 1
AAZ92037
ID AAZ92037 standard; DNA; 21 BP.
XX
AC AAZ92037;
XX
DT 08-JUN-2000 (first entry)
XX
DE STATS binding sequence oligonucleotide MGPe.
XX
KW STATS protein; signal transducer and activator of transcription 5;
KW protein binding sequence; transcription factor modulator; inhibitor;
KW malignant cell removal; proliferative malignancy; neoplastic disease;
KW immunological disorder; inflammatory disorder; therapy; ds.
XX
OS Synthetic.
XX
PN WO200006696-A2.
XX
PD 10-FEB-2000.
XX
PF 30-JUL-1999; 99WO-US17366.
XX
PR 30-JUL-1998; 98US-0094695.
XX

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PA (UYSF-) UNIV SOUTH FLORIDA.
XX
PI Zuckerman KS, Liu RY;
XX
DR WPI; 2000-195281/17.
XX
PT Therapeutic agent for treating transcription factor-related illnesses
PT such as proliferative malignancies, comprises an oligonucleotide for
PT regulating transcription factor function -
XX
PS Claim 15; Page 34; 43pp; English.
XX
CC This sequence represents a STATS (signal transducer and activator of
CC transcription 5) protein binding sequence. The invention relates to a
CC therapeutic agent comprising an effective amount of an oligonucleotide
CC (1) for modulating the function of transcription factors and a
CC pharmaceutical acceptable carrier. The oligonucleotides can be used in a
CC method of removing malignant cells in vitro. The oligonucleotides can be
CC used in compositions to inhibit transcription factors in illnesses where
CC transcription factors play a role, especially proliferative malignancies,
CC neoplastic diseases, and immunological and inflammatory disorders.
XX
SQ Sequence 21 BP; 8 A; 3 C; 3 G; 7 T; 0 other;
XX
Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGATTCTACGAATTCATTC 21
DB 1 AGATTCTACGAATTCATTC 21
RESULT 2
AAV46012
ID AAV46012 standard; DNA; 20 BP.
XX
AC AAV46012;
XX
DT 16-OCT-1998 (first entry)
XX
DE Immune adjuvant STATS.
XX
KW Immune system; adjuvant; vaccine; cancer; prophylactic; pathogenicity;
KW modulator; tolerance; regulator; helper cell; antigen; immunoglobulin;
KW Ig class; autoimmune response; T-cell; B-cell; tumour; ss.
XX
OS Class Bacteria.
XX
PN EP855184-A1.
XX
PD 29-JUL-1998.
XX
PE 23-JAN-1997; 97EP-0101019.
XX
PR 23-JAN-1997; 97EP-0101019.
XX
PA (HEEG/) HEEG K.
PA (LIPF/) LIPFORD G B.
PA (WAGN/) WAGNER H.
XX
PI Heeg K, Lipford GB, Wagner H;
XX
DR WPI; 1998-389630/34.
XX
PT Antigenic composition comprises polynucleotide fragment and antigen
PT - used as vaccine to treat or prevent e.g. cancer or pathogen
PT infections and to modulate immune response e.g. tolerance break and
PT regulation of TH1/TH2 cells
XX
PS Example 5; Page 9; 28pp; English.
XX
AAV45993-V46019 are fragments of bacterial polynucleotides which are

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CC used as immune adjuvants for inclusion into vaccines to treat cancer and
CC for prophylaxis and/or treatment of conditions caused by pathogenic
CC micro-organisms. The polynucleotide is used for modulation of an immune
CC response and the modulation is selected from the group break of
CC tolerance, regulation of TH1/TH2 helper cell responses, switch of Ig
CC classes, treatment of autoimmune responses and induction of tolerances.
CC DNA oligomers are used to enhance the reactivity of immune cells to
CC viral, bacterial and parasitic antigens, to break tolerance in anergic T
CC and B cells e.g. against tumour antigens, as adjuvants in vaccination
CC against tumour-defined antigens and immunostimulatory substances in an
CC immune response against tumours and to suppress immune reactions of the
CC innate and acquired immune system. The composition is inexpensive and
CC stable and does not cause lethal shock, which happens with prior art
CC bacterial sequences.

CC Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 other;

Query Match 85.7%; Score 18; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCAA 18
DB 1 AGATTCTAGGAATTCAA 18

RESULT 3
ID AAL39155 AAL39155 standard; DNA; 20 BP.

AC AAL39155;

DT 05-SEP-2002 (first entry)

DE Murine Toll-like receptor related Cpg DNA SEQ ID No 30.

KM Murine Toll-like receptor; TLR3; TLR7; TLR8; ISNA; ds.

XX Unidentified.

PN WO200222809-A2.

PD 21-MAR-2002.

PF 17-SEP-2001; 2001WO-US29229.

PR 15-SEP-2000; 2000US-233035P.

PR 23-JUN-2001; 2001US-263657P.

PR 17-MAY-2001; 2001US-291726P.

PR 22-JUN-2001; 2001US-300210P.

PA (COLE-) COLEY PHARM GMBH.

PI Bauer S, Liford G, Wagner H;

DR WPI; 2002-393964/42.

PS Disclosure; Page 76; 195pp; English.

CC The invention relates to isolated murine Toll-like receptors (TLR) 9,
CC TLR7 and TLR8 polypeptides. These polypeptides comprise fully defined
CC sequences of 1032, 1050 or 1032 amino acids as given in specification, or
CC their fragments, where TLR9, TLR7 and TLR8 polypeptides or their
CC fragments have an amino acid sequence which is identical to human TLR9,
CC TLR7 or TLR8 polypeptides or their fragment except for at least one amino
CC acid of a murine TLR polypeptide. The isolated nucleic acids of the
CC invention are useful for inhibiting TLR9 signalling activity in a cell.
CC TLR7, TLR8 and TLR9 polypeptides are useful for identifying nucleic acid
CC molecules which interact with a TLR polypeptide or its fragment. The

CC TLR7, TLR8 or TLR9 polypeptides are also useful for identifying ISNA. The
CC signalling activity of a test compound (that is not a nucleic acid, and
CC is a polypeptide or a part of a combinatorial library of compounds) with
CC an ISNA. The TLR7, TLR8 and TLR9 polypeptides are also useful for
CC identifying species specificity of an ISNA. The isolated nucleic acids of
CC the invention are useful as probes or primers. This polynucleotide
CC sequence represents DNA relating to the isolated Toll-like receptors of
CC the invention.

CC Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 other;

Query Match 85.7%; Score 18; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCAA 18
DB 1 AGATTCTAGGAATTCAA 18

RESULT 4
ID ABT17264 ABT17264 standard; DNA; 21 BP.

AC ABT17264;

DT 10-APR-2003 (first entry)

DE Transcription factor probe - SEQ ID No 91.

KM Probe; ss; transcription factor-protein complex; transcription factor;
KM drug screening; drug identification; array hybridisation.

XX Unidentified.

PN WO2002101351-A2.

PD 19-DEC-2002.

PF 30-MAY-2002; 2002WO-US17408.

PR 08-JUN-2001; 2001US-0877243.

PR 08-JUN-2001; 2001US-0877403.

PR 08-JUN-2001; 2001US-0877705.

PR 05-SEP-2001; 2001US-0947274.

PA (PANO-) PANOMICS INC.

PI Li X;

DR WPI; 2003-148829/14.

CC Identifying transcription factor-protein complexes, by isolating
CC transcription factor complexes from sample based on a specific type of
CC factor, and identifying different proteins present in isolated
CC complexes -
CC Disclosure; Fig 6; 167pp; English.

CC The invention comprises a method for identifying complexes between a
CC transcription factor and another protein. The invention also comprises a
CC method for isolating DNA probes which bind to activated transcription
CC factors. The methods of the invention are useful for identifying
CC transcription factor-protein interactions. The methods of the invention
CC are also useful for facilitating the screening and identification of new
CC drugs, characterising their mechanism of action and screening for adverse
CC side effects based on drug's impact expression. The present DNA sequence
CC represents a probe used in the method of the invention.

CC Sequence 21 BP; 7 A; 4 C; 3 G; 7 T; 0 other;

Query Match 85.7%; Score 18; DB 25; Length 21;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
 |||||
 DB 1 AGATTCTAGGAATTCAA 18

RESULT 5

ABT17265/c
 ID ABT17265 standard; DNA; 21 BP.

XX ABT17265;

DT 10-APR-2003 (first entry)

DE Transcription factor probe - SEQ ID No 92.

XX Probe; ss: transcription factor-protein complex; transcription factor;
 KM drug screening; drug identification; array hybridisation.

XX Unidentified.

XX WO2002101351-A2.

XX 19-DEC-2002.

PF 30-MAY-2002; 2002WO-US17408.

PR 08-JUN-2001; 2001US-0877243.

PR 08-JUN-2001; 2001US-0877403.

PR 08-JUN-2001; 2001US-0877705.

PR 08-JUN-2001; 2001US-0877738.

PR 05-SEP-2001; 2001US-0947274.

PA (PANO-) PANOMICS INC.

XX L1 X;

XX WPI; 2003-148829/14.

XX Identifying transcription factor-protein complexes, by isolating
 PT transcription factor complexes from sample based on a specific type of
 PT factor, and identifying different proteins present in isolated
 PT complexes

XX Disclosure; Fig 6; 167bp; English.

XX The invention comprises a method for identifying complexes between a
 CC transcription factor and another protein. The invention also comprises a
 CC method for isolating DNA probes which bind to activated transcription

CC factors. The methods of the invention are useful for identifying
 CC transcription factor-protein interactions. The methods of the invention

CC are also useful for facilitating the screening and identification of new
 CC drugs, characterising their mechanism of action and screening for adverse
 CC side effects based on drug's impact expression. The present DNA sequence
 CC represents a probe used in the method of the invention.

XX Sequence 21 BP; 7 A; 3 C; 4 G; 7 T; 0 other;

XX Query Match 85.7%; Score 18; DB 25; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 72;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
 |||||
 DB 21 AGATTCTAGGAATTCAA 4

XX 21 AGATTCTAGGAATTCAA 4

XX 21 AGATTCTAGGAATTCAA 4

XX 21 AGATTCTAGGAATTCAA 4

XX 21 AGATTCTAGGAATTCAA 4

XX 21 AGATTCTAGGAATTCAA 4

XX 21 AGATTCTAGGAATTCAA 4

XX AC ABT17327;
 XX DT 10-APR-2003 (first entry)
 XX DE Transcription factor-related array hybridisation probe - SEQ ID No 154.
 XX Probe; ss: transcription factor-protein complex; transcription factor;
 KM drug screening; drug identification; array hybridisation.

XX Unidentified.

XX WO2002101351-A2.

XX 19-DEC-2002.

PF 30-MAY-2002; 2002WO-US17408.

PR 08-JUN-2001; 2001US-0877243.

PR 08-JUN-2001; 2001US-0877403.

PR 08-JUN-2001; 2001US-0877705.

PR 08-JUN-2001; 2001US-0877738.

PR 03-SEP-2001; 2001US-0947274.

PA (PANO-) PANOMICS INC.

XX L1 X;

XX WPI; 2003-148829/14.

XX Identifying transcription factor-protein complexes, by isolating
 PT transcription factor complexes from sample based on a specific type of
 PT factor, and identifying different proteins present in isolated
 PT complexes

XX Disclosure; Fig 6; 167bp; English.

XX The invention comprises a method for identifying complexes between a
 CC transcription factor and another protein. The invention also comprises a
 CC method for isolating DNA probes which bind to activated transcription

CC factors. The methods of the invention are useful for identifying
 CC transcription factor-protein interactions. The methods of the invention

CC are also useful for facilitating the screening and identification of new
 CC drugs, characterising their mechanism of action and screening for adverse
 CC side effects based on drug's impact expression. The present DNA sequence
 CC represents a probe used in the method of the invention.

XX Sequence 63 BP; 21 A; 9 C; 12 G; 21 T; 0 other;

XX Query Match 85.7%; Score 18; DB 25; Length 63;
 XX Best Local Similarity 100.0%; Pred. No. 75;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
 |||||
 DB 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

XX 63 AGATTCTAGGAATTCAA 46

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XX OS Synthetic.
XX PN WO200068381-A1.
XX PD 16-NOV-2000.
XX PF 11-MAY-2000; 2000WO-US12924.
XX PR 11-MAY-1999; 99US-0309861.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Presnell SR, Foster DC, Hammond AK, Lok S;
XX DR WPI; 2001-016096/02.
XX PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
XX PT that stimulate proliferation or development of haematopoietic,
XX PT lymphoid and myeloid cells
XX PS
XX PS Example 19; Page 128; 134pp; English.
CC Isolating a nucleotide which encodes the zcytor 10 cytokine
CC receptor enables the production of recombinant cells expressing the
CC receptor. Those cells can then be used to detect the presence of a
CC modulator of zcytor10 protein by culturing the cells in the presence
CC of a test ligand and comparing levels of activity of mouse zcytor10
CC in the presence and absence of the test sample. Similarly, detection
CC of zcytor10 receptor ligand within a test sample can be achieved.
CC The method comprising contacting a test sample containing an amino
CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC cytokine receptor and detecting the binding of the polypeptide to a
CC ligand in the sample. Specified peptide fragments of the zcytor 10
CC cytokine receptor and the methods described are used to identify
CC ligands that stimulate the proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC the cytokine receptor are useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders and for generating
CC antibodies directed against the receptor. An exemplary luciferase
CC mammalian expression vector is the K2134 plasmid which was
CC constructed with two complementary oligonucleotides (AAAs4479,
CC AAAs4480) which comprise STAT transcription factors from 4 genes
CC (a modified c-fos 5'is element, the p21 S1B1 from the p21 WAF1
CC gene, the mammary gland response element of the beta-casein gene
CC and a STAT inducible element of the Fcg RI gene.
XX SQ
SQ Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;
Query Match 85.7%; Score 18; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AGATTCTAGGAATTCAA 18
DB 67 AGATTCTAGGAATTCAA 84
RESULT 8
AAAs4480/c
ID AAAs4480 standard; DNA; 100 BP.
XX AC AAAs4480;
XX DT 11-APR-2001 (first entry)
XX DE DNA fragment comprising STAT transcription factors.
XX KM zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
XX KM binding; detection; modulation; recombinant cell;
XX KM haematopoietic cell; lymphoid cell; myeloid cell; lymph;
XX KM immune system; blood; bone; inflammatory response; inflammation;
XX KM spleen; human; primer; ss.
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XX OS Synthetic.
XX PN WO200068381-A1.
XX PD 16-NOV-2000.
XX PF 11-MAY-2000; 2000WO-US12924.
XX PR 11-MAY-1999; 99US-0309861.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Presnell SR, Foster DC, Hammond AK, Lok S;
XX DR WPI; 2001-016096/02.
XX PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
XX PT that stimulate proliferation or development of haematopoietic,
XX PT lymphoid and myeloid cells
XX PS
XX PS Example 19; Page 128; 134pp; English.
CC Isolating a nucleotide which encodes the zcytor 10 cytokine
CC receptor enables the production of recombinant cells expressing the
CC receptor. Those cells can then be used to detect the presence of a
CC modulator of zcytor10 protein by culturing the cells in the presence
CC of a test ligand and comparing levels of activity of mouse zcytor10
CC in the presence and absence of the test sample. Similarly, detection
CC of zcytor10 receptor ligand within a test sample can be achieved.
CC The method comprising contacting a test sample containing an amino
CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC cytokine receptor and detecting the binding of the polypeptide to a
CC ligand in the sample. Specified peptide fragments of the zcytor 10
CC cytokine receptor and the methods described are used to identify
CC ligands that stimulate the proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC the cytokine receptor are useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders and for generating
CC antibodies directed against the receptor. An exemplary luciferase
CC mammalian expression vector is the K2134 plasmid which was
CC constructed with two complementary oligonucleotides (AAAs4479,
CC AAAs4480) which comprise STAT transcription factors from 4 genes
CC (a modified c-fos 5'is element, the p21 S1B1 from the p21 WAF1
CC gene, the mammary gland response element of the beta-casein gene
CC and a STAT inducible element of the Fcg RI gene.
XX SQ
SQ Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;
Query Match 85.7%; Score 18; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AGATTCTAGGAATTCAA 18
DB 38 AGATTCTAGGAATTCAA 21
RESULT 9
ABA93801
ID ABA93801 standard; DNA; 100 BP.
XX AC ABA93801;
XX DT 01-MAY-2002 (first entry)
XX DE K2134 plasmid construction oligonucleotide SEQ ID NO:43.
XX KM Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
XX KM antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
XX KM muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
XX KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
XX KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
```

KM inflammatory disease; pancreatitis; inflammatory bowel disease;
KM PCR primer, probe; ss.
XX
OS Synthetic.
XX
PN W0200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
PR 29-JUN-2000; 2000US-214955P.
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer WF;
XX
PT WPI; 2002-090519/12.
XX
DR Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX
PS Example 19; Page 190; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,
CC antineumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopemias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. Crohn's disease), cancer,
CC sclerostis), inflammatory diseases (e.g. rheumatoid arthritis and multiple
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;
Query Match 85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGATTCTAGCAATTCAA 18
DB 67 AGATTCTAGCAATTCAA 84
|||||
RESULT 10
ID ABA93802/C
ID ABA93802 standard; DNA, 100 BP.
XX
AC ABA93802;
XX
DT 01-MAY-2002 (first entry)
XX
DE K2134 plasmid construction oligonucleotide SEQ ID NO:44.
XX
KM Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KM antiinflammatory; antiviral; antirheumatic; antiarthritic; cyostatic;
KM muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KM autoimmune disease; rheumatoid arthritis; multiple sclerostis; cancer;
KM inflammatory disease; pancreatitis; inflammatory bowel disease;
KM PCR primer; probe; ss.

XX
OS Synthetic.
XX
PN W0200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
PR 29-JUN-2000; 2000US-214955P.
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer WF;
XX
PT WPI; 2002-090519/12.
XX
DR Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX
PS Example 19; Page 190; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,
CC antineumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopemias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. Crohn's disease), cancer,
CC sclerostis), inflammatory diseases (e.g. rheumatoid arthritis and multiple
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;
Query Match 85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGATTCTAGCAATTCAA 18
DB 38 AGATTCTAGCAATTCAA 21
|||||
RESULT 11
ID AAS20691
ID AAS20691 standard; DNA, 100 BP.
XX
AC AAS20691;
XX
DT 09-APR-2002 (first entry)
XX
DE Plasmid K2 134 oligonucleotide ZC12749.
XX
KM Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
KM natural killer cell proliferation; T-cell proliferation;
KM B-cell proliferation; anti-tumour response; immune system;
KM immunostimulant; cyostatic; primer; ss.
XX
OS Synthetic.
XX
PN US6307024-B1.

23-OCT-2001.
XX
XX 09-MAR-2000; 2000US-0522217.
PF
XX 09-MAR-1999; 99US-123547P.
PR 11-MAR-1999; 99US-123904P.
PR 01-JUL-1999; 99US-142013P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
DR WPI; 2002-040208/05.
XX
XX New zalphal1 ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response -
XX
XX Example 20; Column 149-150; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
CC zalphal1 ligand and the polynucleotide encoding it. The invention
CC also gives the sequence for the zalphal1 receptor and the polynucleotide
CC encoding it. The zalphal1 ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated
CC with anti-CD40 antibodies, stimulates an antigenic response in a mammal,
CC and reduces proliferation of B-cells stimulated with anti-IgM antibodies.
CC The zalphal1 ligand polypeptide is also useful in preparing antibodies
CC that bind to zalphal1 ligand epitopes. The zalphal1 ligand
CC polynucleotides can be used as probes or primers to clone regions
CC of a zalphal1 ligand gene, and in gene therapy. Zalphal1 ligand may
CC also be used to identify inhibitors of its activity, to enhance the
CC generation of anti-tumour responses with or without the infusion of
CC donor lymphocytes, and to activate or stimulate the immune system.
CC The present sequence represents an oligonucleotide used to construct
CC plasmid KZ 134 in the methods of the present invention.
XX
SQ Sequence 100 BP; 25 A; 32 C; 17 G; 26 T; 0 other;
XX
Query Match 85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGATTTCAGGAATTCAA 18
DB 67 AGATTTCAGGAATTCAA 84
RESULT 12
AAS20692/c
ID AAS20692 standard; DNA; 100 BP.
XX
AC AAS20692;
XX
DT 09-APR-2002 (first entry)
XX
DE Plasmid KZ 134 oligonucleotide ZC12748.
XX
XX Cytokine; zalphal1 ligand; zalphal1 receptor; NK cell progenitor;
KM natural killer cell proliferation; T-cell proliferation;
KM B-cell proliferation; anti-tumour response; immune system;
KM immunostimulant; cytostatic; primer; ss.
XX
OS Synthetic.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-0522217.

XX
XX 09-MAR-1999; 99US-123547P.
PR 11-MAR-1999; 99US-123904P.
PR 01-JUL-1999; 99US-142013P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
DR WPI; 2002-040208/05.
XX
XX New zalphal1 ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response -
XX
XX Example 20; Column 149-151; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
CC zalphal1 ligand and the polynucleotide encoding it. The invention
CC also gives the sequence for the zalphal1 receptor and the polynucleotide
CC encoding it. The zalphal1 ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated
CC with anti-CD40 antibodies, stimulates an antigenic response in a mammal,
CC and reduces proliferation of B-cells stimulated with anti-IgM antibodies.
CC The zalphal1 ligand polypeptide is also useful in preparing antibodies
CC that bind to zalphal1 ligand epitopes. The zalphal1 ligand
CC polynucleotides can be used as probes or primers to clone regions
CC of a zalphal1 ligand gene, and in gene therapy. Zalphal1 ligand may
CC also be used to identify inhibitors of its activity, to enhance the
CC generation of anti-tumour responses with or without the infusion of
CC donor lymphocytes, and to activate or stimulate the immune system.
CC The present sequence represents an oligonucleotide used to construct
CC plasmid KZ 134 in the methods of the present invention.
XX
SQ Sequence 100 BP; 26 A; 17 C; 32 G; 25 T; 0 other;
XX
Query Match 85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGATTTCAGGAATTCAA 18
DB 38 AGATTTCAGGAATTCAA 21
RESULT 13
AAD22953
ID AAD22953 standard; DNA; 100 BP.
XX
AC AAD22953;
XX
DT 26-FEB-2002 (first entry)
XX
DE BaF3/KZ134/zalphal1 cell line constructing ZC12,749 oligonucleotide.
XX
XX Zalphal1; cytokine receptor; immunosuppressive; cytostatic; haemostatic;
KM inflammatory disorder; cell proliferation; immune disorder; cancer; SLE;
KM systemic lupus erythematosus; myasthenia gravis; rheumatoid arthritis;
KM diabetes; autoimmune disease; multiple sclerosis; ulcerative colitis;
KM inflammatory bowel disease; sepsis; Crohn's disease; viral infection;
KM asthma; ss.
XX
OS Unidentified.
XX
PN WO200177171-A2.
XX
PD 18-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10872.
XX

```

PR 05-APR-2000; 2000US-194731P.
PR 28-JUL-2000; 2000US-222121P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sprecher CA, Novak UE, West JW, Presnell SR, Holly RD, Nelson AJ;
XX WPI; 2002-025898/03.
XX
PT Novel soluble receptor polypeptides and polynucleotides used as
PT cytokine antagonist for stimulating ligand activity-induced
PT proliferation of hematopoietic cells and for suppressing immune
PT response in a mammal
XX
PS Example 19; Page 213; 243pp; English.
XX
CC The invention relates to an isolated soluble zalphail cytokine receptor
CC polypeptide and their cDNA molecules. Zalpha proteins are useful for
CC inhibiting or antagonising the ligand activity-induced proliferation of
CC hematopoietic cells and hematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalpha is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
CC useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is an oligonucleotide used for Baf3/KZ134/zalphail cell line
CC construction.
XX
SQ Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;

Query Match      85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 67 AGATTCTAGGAATTCAA 84

RESULT 14
AAD22954/c
ID AAD22954 standard; DNA; 100 BP.
XX
AC AAD22954;
XX
DT 26-FEB-2002 (first entry)
XX
DE Baf3/KZ134/zalphail cell line constructing ZC12,748 oligonucleotide.
XX
KW Zalphail; cytokine receptor; immunosuppressive; cytostatic; hemostatic;
KW inflammatory disorder; cell proliferation; immune disorder; cancer; SLE;
KW systemic lupus erythematosus; myasthenia gravis; rheumatoid arthritis;
KW diabetes; autoimmune disease; multiple sclerosis; ulcerative colitis;
KW inflammatory bowel disease; sepsis; Crohn's disease; viral infection;
KW asthma; ss.
XX
OS Unidentified.
XX
PN WO200177171-A2.
XX
PD 18-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10872.
XX
PR 05-APR-2000; 2000US-194731P.
PR 28-JUL-2000; 2000US-222121P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX

```

```

PI Sprecher CA, Novak UE, West JW, Presnell SR, Holly RD, Nelson AJ;
XX WPI; 2002-025898/03.
XX
PT Novel soluble receptor polypeptides and polynucleotides used as
PT cytokine antagonist for stimulating ligand activity-induced
PT proliferation of hematopoietic cells and for suppressing immune
PT response in a mammal
XX
PS Example 19; Page 213; 243pp; English.
XX
CC The invention relates to an isolated soluble zalphail cytokine receptor
CC polypeptide and their cDNA molecules. Zalpha proteins are useful for
CC inhibiting or antagonising the ligand activity-induced proliferation of
CC hematopoietic cells and hematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalpha is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
CC useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is an oligonucleotide used for Baf3/KZ134/zalphail cell line
CC construction.
XX
SQ Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;

Query Match      85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 38 AGATTCTAGGAATTCAA 21

RESULT 15
ABK88204/c
ID ABK88204 standard; DNA; 33 BP.
XX
AC ABK88204;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human cytochrome bcl core protein cDNA specific PCR primer #2.
XX
KW Cytochrome bcl; primer; ss; core protein IT12. 21; cancer; HIV;
KW human immunodeficiency virus; human; PCR.
XX
OS Homo sapiens.
XX
PN CN1340524-A.
XX
PD 20-MAR-2002.
XX
PF 31-AUG-2000; 2000CN-0119831.
XX
PR 31-AUG-2000; 2000CN-0119831.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
PD WPI; 2002-436418/47.
XX
PF Polypeptide-human cytochrome bcl compound core protein II 12.21 and
PF polynucleotide for coding it -
XX
PS Example 4; Page 19 (disclosure); 34pp; Chinese.
XX
CC This invention relates to the cDNA and protein sequences of a novel

```

CC polypeptide-human cytochrome bcl compounds core protein I112.21. The
 CC invention also comprises a method for producing the protein by
 CC recombinant DNA technology and a method for the application of the
 CC polypeptide in treating diseases such as cancer, HIV infection, etc.
 CC The invention also discloses an antagonist against this polypeptide and
 CC its therapeutic action, and the application of the polynucleotide to
 CC coding this new human cytochrome bcl compound core protein I112.21.
 CC The present sequence represents a PCR primer used to clone the human
 CC cytochrome bcl compound core protein I112.21 cDNA of the invention.

XX Sequence 33 BP; 10 A; 10 C; 4 G; 9 T; 0 other;

Query Match 76.2%; Score 16; DB 24; Length 33;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGATTTCAGGAATTC 16
 |||||
 DB 19 AGATTTCAGGAATTC 4

RESULT 16

ABL31609
 ID AAL31609 standard; DNA; 51 BP.

AC AAL31609;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #4817.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 PS Claim 1; Page 2773; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include

CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

XX Sequence 51 BP; 22 A; 6 C; 8 G; 15 T; 0 other;

Query Match 73.3%; Score 15.4; DB 22; Length 51;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ATTTCTAGGAATTC 19
 |||||
 DB 9 ATTTCTAGGAATTC 25

RESULT 17

ABL53039/c
 ID ABL53039 standard; DNA; 41 BP.

AC ABL53039;

DT 29-MAY-2002 (first entry)

DE Oligonucleotide JCA 325.

XX Virucide; vaccine; foot and mouth disease; P1 region; capsid;
 KW 3C protease; ds.

XX Foot and mouth disease virus.

XX WO200200251-A1.

XX 03-JAN-2002.

XX 27-JUN-2001; 2001WO-FR02042.

XX 29-JUN-2000; 2000FR-0008437.

XX (MERI-) MERIAL.

XX King A, Burman A, Audonnet J, Lombard M;

DR WPI; 2002-130837/17.

XX Stable, potent effective vaccines against foot-and-mouth disease,
 PT comprises recombinantly produced empty virus capsids as antigens -
 PS Example 7; Page 29; 79pp; French.

XX The present invention relates to a vaccine against foot and mouth disease
 CC (FMD) comprising (in addition to a veterinary vehicle or excipient) an
 CC antigen consisting of empty FMD virus capsids, obtained by expression in
 CC eukaryotic cells of the cDNA of the following regions of the FMD genome:
 CC the P1 region encoding the capsid and the region encoding the 3C
 CC protease. The vaccine is effective, reliable and stable, and is effective
 CC at low doses. The vaccine is useful against foot and mouth disease,
 CC especially in cows, sheep, pigs or goats. The present sequence is an
 CC oligonucleotide which was used in an example from the invention.

XX Sequence 41 BP; 13 A; 7 C; 6 G; 15 T; 0 other;

Query Match 70.5%; Score 14.8; DB 24; Length 41;
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATTTCAGGAATTC 19
 |||||
 DB 19 GATTTCAGGAATTC 2

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RESULT 18
ABL53041/c
ID ABL53041 standard; DNA: 41 BP.
XX
XX
AC ABL53041;
XX
XX
DT 29-MAY-2002 (first entry)
XX
XX
DE Oligonucleotide JCA 327.
XX
XX
KM virucide; vaccine; foot and mouth disease; P1 region; capsid;
XX
XX
KW 3C protease; ds.
XX
XX
OS Foot and mouth disease virus.
XX
XX
PN WO200200251-A1.
XX
XX
PD 03-JAN-2002.
XX
XX
PF 27-JUN-2001; 2001WO-FR02042.
XX
XX
PR 29-JUN-2000; 2000FR-0008437.
XX
XX
PA (MERI-) MERTAL.
XX
XX
PI King A, Burman A, Audonnet J, Lombard M;
XX
XX
DR WPI; 2002-130837/17.
XX
XX
PT Stable, potent effective vaccines against foot-and-mouth disease,
XX
XX
PS comprises recombinantly produced empty virus capsids as antigens
XX
XX
Example 7; Page 30; 79pp; French.
XX
XX
CC The present invention relates to a vaccine against foot and mouth disease
XX
XX
CC (FMD) comprising (in addition to a veterinary vehicle or excipient) an
XX
XX
CC antigen consisting of empty FMD virus capsids, obtained by expression in
XX
XX
CC eukaryotic cells of the cDNA of the following regions of the FMD genome:
XX
XX
CC the P1 region encoding the capsid and the region encoding the 3C
XX
XX
CC protease. The vaccine is effective, reliable and stable, and is effective
XX
XX
CC at low doses. The vaccine is useful against foot and mouth disease,
XX
XX
CC especially in cows, sheep, pigs or goats. The present sequence is an
XX
XX
CC oligonucleotide which was used in an example from the invention.
XX
XX
SQ Sequence 41 BP; 13 A; 6 C; 6 G; 16 T; 0 other;
XX
XX
Query Match 70.5%; Score 14.8; DB 24; Length 41;
XX
XX
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
XX
XX
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 2 GATTTCAGGAATTCANA 19
XX
XX
DB 19 GATTTTATGAAATTCANA 2
XX
XX
RESULT 19
ABL53037/c
ID ABL53037 standard; DNA: 44 BP.
XX
XX
AC ABL53037;
XX
XX
DT 29-MAY-2002 (first entry)
XX
XX
DE Oligonucleotide JCA 323.
XX
XX
KM virucide; vaccine; foot and mouth disease; P1 region; capsid;
XX
XX
KW 3C protease; ds.
XX
XX
OS Foot and mouth disease virus.
XX
XX
PN WO200200251-A1.
XX
XX
PD 03-JAN-2002.

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XX
XX
XX 27-JUN-2001; 2001WO-FR02042.
XX
XX
XX 29-JUN-2000; 2000FR-0008437.
XX
XX
XX (MERI-) MERTAL.
XX
XX
XX King A, Burman A, Audonnet J, Lombard M;
XX
XX
XX WPI; 2002-130837/17.
XX
XX
XX Stable, potent effective vaccines against foot-and-mouth disease,
XX
XX
XX comprises recombinantly produced empty virus capsids as antigens
XX
XX
XX Example 6; Page 26; 79pp; French.
XX
XX
CC The present invention relates to a vaccine against foot and mouth disease
XX
XX
CC (FMD) comprising (in addition to a veterinary vehicle or excipient) an
XX
XX
CC antigen consisting of empty FMD virus capsids, obtained by expression in
XX
XX
CC eukaryotic cells of the cDNA of the following regions of the FMD genome:
XX
XX
CC the P1 region encoding the capsid and the region encoding the 3C
XX
XX
CC protease. The vaccine is effective, reliable and stable, and is effective
XX
XX
CC at low doses. The vaccine is useful against foot and mouth disease,
XX
XX
CC especially in cows, sheep, pigs or goats. The present sequence is an
XX
XX
CC oligonucleotide which was used in an example from the invention.
XX
XX
SQ Sequence 44 BP; 13 A; 7 C; 7 G; 17 T; 0 other;
XX
XX
Query Match 70.5%; Score 14.8; DB 24; Length 44;
XX
XX
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
XX
XX
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 2 GATTTCAGGAATTCANA 19
XX
XX
DB 19 GATTTTATGAAATTCANA 2
XX
XX
RESULT 20
ABL53043/c
ID ABL53043 standard; DNA: 44 BP.
XX
XX
AC ABL53043;
XX
XX
DT 29-MAY-2002 (first entry)
XX
XX
DE Oligonucleotide JCA 329.
XX
XX
KM virucide; vaccine; foot and mouth disease; P1 region; capsid;
XX
XX
KW 3C protease; ds.
XX
XX
OS Foot and mouth disease virus.
XX
XX
PN WO200200251-A1.
XX
XX
PD 03-JAN-2002.
XX
XX
PF 27-JUN-2001; 2001WO-FR02042.
XX
XX
PR 29-JUN-2000; 2000FR-0008437.
XX
XX
PA (MERI-) MERTAL.
XX
XX
PI King A, Burman A, Audonnet J, Lombard M;
XX
XX
XX WPI; 2002-130837/17.
XX
XX
XX Stable, potent effective vaccines against foot-and-mouth disease,
XX
XX
XX comprises recombinantly produced empty virus capsids as antigens
XX
XX
XX Example 7; Page 30; 79pp; French.
XX
XX
CC The present invention relates to a vaccine against foot and mouth disease
XX
XX
CC (FMD) comprising (in addition to a veterinary vehicle or excipient) an

```

CC antigen consisting of empty FMD virus capsids, obtained by expression in
CC eukaryotic cells of the cDNA of the following regions of the FMD genome:
CC the P1 region encoding the capsid and the region encoding the 3C
CC protease. The vaccine is effective, reliable and stable, and is effective
CC at low doses. The vaccine is useful against foot and mouth disease,
CC especially in cows, sheep, pigs or goats. The present sequence is an
CC oligonucleotide which was used in an example from the invention.
XX
SQ Sequence 44 BP; 12 A; 10 C; 9 G; 13 T; 0 other;

Query Match 70.5%; Score 14.8; DB 24; Length 44;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATTTCCTAGGAATTCAAA 19
19 GATTTCCTAGGAATTCAAA 2

Db

RESULT 21
AAZ23234/C
ID AAZ23234 standard; DNA; 46 BP.
XX
AC AAZ23234;
XX
DT 24-JAN-2000 (first entry)
XX
DE HCV NS5B gene amplifying nested primer.
XX
KW Hepatitis C virus; HCV; non-structural 5B; viral antigen; antiviral;
KW immune response; diagnostic; therapeutic; pharmaceutical; NS5B;
KW PCR primer; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN WO9951781-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US07404.
XX
PR 02-APR-1998; 98US-0080509.
PR 23-JUN-1998; 98US-0090356.
XX
PA (VIRCO-) VITROPHARMA INC.
XX
PI Collect MS;
XX
DR WPI; 1999-620215/53.
XX
PT Novel protein and polynucleotides used in diagnostic assays and
PT therapeutic treatments for Hepatitis C virus -
XX
PS Example 1; Page 47; 129pp; English.
XX
CC The invention provides nucleic acid molecules encoding hepatitis C virus
CC (HCV) non-structural 5B (NS5B) proteins. The HCV NS5B protein can be
CC used in assays to determine antagonistic or agonistic activity of test
CC compounds against HCV. HCV can be detected in biological samples by
CC amplification of the NS5B coding sequence and detection using an
CC oligonucleotide probe (derived from the NS5B nucleotide sequence). The
CC HCV NS5B protein is a viral antigen and can be used in raising an immune
CC response in a mammalian subject. Cell lines comprising the HCV NS5B
CC nucleic acid sequence can be used to assess the functionality of the
CC protein and for assaying test compounds for antagonistic or agonistic
CC activity. The HCV NS5B protein and nucleic acid sequences are useful in
CC research, diagnostic, therapeutic and pharmaceutical applications, and
CC for use in assays for the identification of efficacious antiviral
CC agents. Sequences AAZ23232-235 represent PCR primers for cloning the HCV
CC NS5B genes.
XX
SQ Sequence 46 BP; 17 A; 9 C; 6 G; 14 T; 0 other;

Query Match 69.5%; Score 14.6; DB 20; Length 46;
Best Local Similarity 81.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCAAATC 21
25 ATATTATTAAGCAATTCAGATC 5

Db

RESULT 22
AAV59344
ID AAV59344 standard; CDNA; 58 BP.
XX
AC AAV59344;
XX
DT 21-DEC-1998 (first entry)
XX
DE zsig10 primer ZC15.632.
XX
SS; human; mucous-mediated function; adhesion; tumour metastasis;
KW bacterial colonisation; microbial infection; AIDS; cystic fibrosis;
KW chronic obstructive pulmonary disease; asthma; Crohn's disease;
KW sinonasal inflammatory disease; inflammatory bowel disease; bronchitis;
KW PCR; primer; amplification.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9841627-A1.
XX
PD 24-SEP-1998.
XX
PF 18-MAR-1998; 98WO-US05251.
XX
PR 19-MAR-1997; 97US-0039631.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO;
XX
DR WPI; 1998-531566/45.
XX
PT New isolated mucous-associated polypeptide, zsig10 - used to develop
PT products for treating e.g. tumour metastasis, microbial infections,
PT cystic fibrosis, asthma, bronchitis or inflammatory bowel disease
XX
PS Example 7; Page 94; 109pp; English.
XX
CC The primers AAV59330-V59351 were used in the production of a human
CC polypeptide zsig10. zsig10 is involved in mucous-mediated functions
CC such as adhesion. The products of the invention can be used in the
CC study and treatment of e.g. tumour metastasis, bacterial colonisation,
CC susceptibility to and persistence of infection, microbial infections,
CC AIDS, cystic fibrosis, chronic obstructive pulmonary disease, asthma,
CC sinonasal inflammatory disease, inflammatory bowel disease, bronchitis,
CC or Crohn's disease. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 58 BP; 17 A; 19 C; 9 G; 13 T; 0 other;

Query Match 69.5%; Score 14.6; DB 19; Length 58;
Best Local Similarity 81.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCAAATC 21
14 AGAATCTAGGAATTCCTACTC 34

Db

RESULT 23
AAX80718
ID AAX80718 standard; DNA; 58 BP.

CC double-stranded, circular DNA molecule, comprising combining
CC donor DNA fragments encoding the protein of interest with an acceptor
CC plasmid, and two DNA linkers in a Saccharomyces cerevisiae host cell. The
CC encoding DNA is linked to the acceptor plasmid by homologous
CC recombination of with the linkers and acceptor plasmid to form the
CC closed, circular plasmid. The obtained plasmid is useful for transforming
CC host cells and producing proteins of interest. The method allows for
CC production of a standardised plasmid into which a variety of DNA
CC sequences can be readily inserted and subsequently expressed.

XX Sequence 58 BP; 17 A; 19 C; 9 G; 13 T; 0 other;

Query Match 69.5%; Score 14.6; DB 22; Length 58;
Best Local Similarity 81.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAATC 21
DB 14 AGAATCTAGGAATTCCTACTC 34

RESULT 26
ABN83120
ID ABN83120 standard; DNA; 58 BP.

XX ABN83120;
AC
XX
XX 11-SEP-2002 (first entry)

DE Human alpha helical protein-1 C-terminal zalphal-CBE linker PCR primer 2.

KW Human; alpha helical protein-1; Zalphal; vasotrophic; dermatological;
KW cyrostatic; antidegenerative; fragile-X syndrome; gene therapy; cancer;
KW blood vessel disease; macroorchidism; skin disorder; joint instability;
KW degeneration; ss; PCR; primer.

XX Homo sapiens.

OS US2002058801-A1.

XX 16-MAY-2002.

PF 16-AUG-2001; 2001US-0932679.

PR 10-DEC-1997; 97US-067779P.

PR 10-DEC-1998; 98US-0209525.

PA (ZYMO) ZYMOGENETICS INC.

PI Lok S, Conklin DC, Parrish JE;

DR WI; 2002-471089/50.

PT New polynucleotide encoding human Zalphal protein, useful e.g. for
PT treating phenotypic traits of fragile-X syndrome, also related
PT polypeptide

PS Example 6; Page 22; 27pp; English.

XX The invention relates to a novel isolated polynucleotide encoding
CC a human alpha helical polypeptide. The polynucleotide of the invention
CC has vasotrophic, dermatological, cyrostatic, and antidegenerative
CC activity. The polynucleotide is used for expressing the protein, for
CC detecting mutations and alterations in transcription of the corresponding
CC gene in fragile-X syndrome patients, and in gene therapy. The polypeptide
CC or its (ant)agonists, are used for treating some of the phenotypic traits
CC associated with fragile-X syndrome, for promoting growth
CC differentiation, maintenance and survival of connective tissues, e.g. for
CC treating blood vessel diseases, macroorchidism, skin disorders and joint
CC instability, also for cosmetic improvement of the skin or also its
CC specific antibodies and anti-idiotypic antibodies, for treating abnormal
CC proliferation, e.g. cancer, and degeneration. The present sequence
CC represents a PCR primer used in the invention to generate the C-terminal

CC zalphal-CBE linker, for the production of a plasmid containing the
CC human alpha helical protein-1 (zalphal) gene.

XX Sequence 58 BP; 17 A; 19 C; 9 G; 13 T; 0 other;

Query Match 69.5%; Score 14.6; DB 24; Length 58;
Best Local Similarity 81.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAATC 21
DB 14 AGAATCTAGGAATTCCTACTC 34

RESULT 27
ABK12090
ID ABK12090 standard; DNA; 58 BP.

XX ABK12090;
AC
XX
XX 05-JUN-2002 (first entry)

DE C-terminal-CBE-zalphal tagged linker oligonucleotide #2.

KW Zalphal; alpha helical protein-1; cyrostatic; gene therapy;
KW abnormal proliferation; cancerous condition; tumour; ss;
KW degenerative condition; C-terminal-CBE-zalphal tagged linker.

OS Synthetic.

XX US6303770-B1.

PD 16-OCT-2001.

PF 10-DEC-1998; 98US-0209525.

PR 10-DEC-1997; 97US-067779P.

PA (ZYMO) ZYMOGENETICS INC.

PI Lok S, Conklin DC, Parrish JE;

DR WI; 2002-235900/29.

PT New polynucleotides encoding mammalian alpha helical protein-1, useful
PT for treating conditions associated with abnormal physiology or
PT development, e.g. proliferative or cancerous conditions, or
PT degenerative conditions

PS Example 6; Column 39; 25pp; English.

XX The present invention relates to a new polynucleotide sequence, Zalphal,
CC which comprises 907 nucleotides, fully defined in the specification, or
CC its portion that encodes a polypeptide. The polypeptide of the invention
CC comprises 146 or 126 amino acids, also fully defined in the
CC specification. The polynucleotide of the invention is useful for
CC providing an encoded polypeptide that may be used for treating conditions
CC associated with abnormal physiology or development e.g. abnormal
CC proliferation (e.g. cancerous conditions) or degenerative conditions.
CC The present nucleic acid sequence represents the C-terminal-CBE-zalphal
CC tagged linker oligonucleotide #2 sequence of the invention. Zalphal is
CC a mammalian alpha helical protein-1.

XX Sequence 58 BP; 17 A; 19 C; 9 G; 13 T; 0 other;

Query Match 69.5%; Score 14.6; DB 24; Length 58;
Best Local Similarity 81.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAATC 21
DB 14 AGAATCTAGGAATTCCTACTC 34

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RESULT 28
XX ABV72202/c
XX ID ABV72202 standard; DNA; 20 BP.
XX AC ABV72202;
XX DT 05-DEC-2002 (first entry)
XX DE Nucleotide sequence of a PCR primer.
XX KM DNA fingerprint; phenotype; polymorphism; MITE; molecular marker;
XX KW miniature inverted repeat transposable element; PCR; primer; ss.
XX OS Zea mays.
XX PN US6420117-B1.
XX PD 16-JUL-2002.
XX PF 14-SEP-2000; 2000US-0662402.
XX PR 14-SEP-1999; 99US-153812P.
XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX PI Wessler SR, Casa AM;
XX DR WPI; 2002-654638/70.
XX DT
XX PT Producing a DNA fingerprint of an individual by amplifying fragments
XX PT containing a miniature inverted repeat transposable element is useful
XX PT to detect polymorphisms and correlate genotype with phenotype
XX PT particularly in maize -
XX PS Disclosure; Column 41; 37bp; English.
XX CC The specification describes a method for producing a DNA fingerprint of
XX CC an individual. The method comprises generating restriction fragments to
XX CC which an adaptor is ligated, amplifying fragments containing a miniature
XX CC inverted repeat transposable element (MITE) and resolving the amplified
XX CC fragments. The presence of a certain amplified fragment is correlated
XX CC to a phenotype. The method is used to characterize the DNA of an
XX CC individual, to detect polymorphisms, to correlate presence of an
XX CC amplified fragment with phenotype and to generate a set of molecular
XX CC markers. The present PCR primer is used in the course of the invention.
XX SQ Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 other;
XX
Query Match 67.6%; Score 14.2; DB 24; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 ATTCTAGGAATTCGAATC 21
Db 19 ATTTCGAGGAATTCGAATC 1

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```

RESULT 29
XX AA164395/c
XX ID AA164395 standard; DNA; 27 BP.
XX AC AA164395;
XX DE PCR primer #2.
XX KM Green fluorescence protein; GFP; drug screening; PCR primer;
XX KW cell organelle formation; ss.
XX OS Unidentified.
XX
Query Match 67.6%; Score 14.2; DB 24; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AGATTCTAGGAATTCGAA 19
Db 19 AGCTAGCTAGGAATTCGAA 1

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RESULT 30
XX AA164405/c
XX ID AA164405 standard; DNA; 27 BP.
XX AC AA164405;
XX DE 23-NOV-2001 (first entry)
XX DT PCR primer #12.
XX DE PCR primer #12.
XX KM Green fluorescence protein; GFP; drug screening; PCR primer;
XX KW cell organelle formation; ss.
XX OS Unidentified.
XX PN JP2001157588-A.
XX PD 12-JUN-2001.
XX PF 02-DEC-1999; 99JP-0343222.
XX PR 02-DEC-1999; 99JP-0343222.
XX PA (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.
XX DR WPI; 2001-592442/67.
XX PT Gene trap using a green fluorescence protein -
XX PS Example 1; Page 7; 17pp; Japanese.
XX CC The present invention relates to a trap vector containing, from 5'- to
XX CC 3'-, an intron and splice acceptor sequence, a DNA sequence encoding
XX CC green fluorescence protein (GFP) in which methionine and valine at the
XX CC N-terminal are deleted, an internal ribosome binding site (IRES), a DNA
XX CC sequence encoding a selective marker, and polyadenylated signal sequence.
XX CC The invention can be used in the screening of drugs inhibiting or
XX CC promoting the formation of cell organelles. The present sequence is a PCR
XX CC primer, which was used in an example from the present invention.
XX SQ Sequence 27 BP; 6 A; 6 C; 7 G; 8 T; 0 other;
XX
Query Match 67.6%; Score 14.2; DB 22; Length 27;
Best Local Similarity 84.2%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AGATTCTAGGAATTCGAA 19
Db 19 AGCTAGCTAGGAATTCGAA 1

```


CC promoting the formation of cell organelles. The present sequence is a PCR
CC primer, which was used in an example from the present invention.
XX

Sequence 27 BP; 6 A; 6 C; 7 G; 8 T; 0 other;

Query Match 67.6%; Score 14.2; DB 22; Length 27;
Best Local Similarity 84.2%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAAATTCAAA 19
DB 19 AGCTAGCTAGGAAATTCAAA 1

RESULT 31

AA176494/c
ID AA176494 standard; DNA; 51 BP.

AA176494;

09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:3435.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

WO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US32758.

30-NOV-1999; 99US-0168138.

29-NOV-2000; 2000US-0726173.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and
therapy -

Claim 1; Page 1102; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide
sequences (I), which contain single nucleotide polymorphisms (SNPs).

AAW53114 to AAW53329 represent peptides related to human polymorphic
polynucleotide sequences. The sequences can be used in gene and protein
therapy, and in vaccine production. (I) and the polypeptides encoded by
them may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate expression of polymorphic polypeptides.

For example, (I) may be used to treat disorders by rectifying mutations
or deletions in a patient's genome that affect the activity of

CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
complementary sequences may also be used as DNA probes in diagnostic

assays to detect and quantitate the presence of similar nucleic acids
in samples, and therefore which patients may be in need of restorative

therapy. The polypeptides encoded by (I) may be used as antigens in the
production of antibodies specific for polymorphic polypeptides. The

antibodies may also be used to down regulate expression and activity.
The antibodies may also be used as diagnostic agents for detecting the

presence of polymorphic polypeptides in samples.

Sequence 51 BP; 17 A; 10 C; 3 G; 21 T; 0 other;

Query Match

67.6%; Score 14.2; DB 22; Length 51;

Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAAATTCAAA 19
DB 34 AGCTTTATGATTCAAA 16

RESULT 32

AAC52964
ID AAC52964 standard; DNA; 61 BP.

AAC52964;

18-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 72962.

Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

23-MAR-1999; 99US-0125788.

25-MAR-1999; 99US-0126264.

29-MAR-1999; 99US-0126785.

01-APR-1999; 99US-0127462.

06-APR-1999; 99US-0128234.

08-APR-1999; 99US-0129845.

16-APR-1999; 99US-0130077.

19-APR-1999; 99US-0130449.

21-APR-1999; 99US-0130510.

23-APR-1999; 99US-0130891.

28-APR-1999; 99US-0131449.

30-APR-1999; 99US-0132048.

30-APR-1999; 99US-0132407.

04-MAY-1999; 99US-0132484.

05-MAY-1999; 99US-0132485.

06-MAY-1999; 99US-0132486.

07-MAY-1999; 99US-0132487.

11-MAY-1999; 99US-0132863.

14-MAY-1999; 99US-0134218.

14-MAY-1999; 99US-0134219.

14-MAY-1999; 99US-0134221.

14-MAY-1999; 99US-0134370.

14-MAY-1999; 99US-0134768.

19-MAY-1999; 99US-0134941.

20-MAY-1999; 99US-0135124.

21-MAY-1999; 99US-0135353.

24-MAY-1999; 99US-0135629.

25-MAY-1999; 99US-0136021.

27-MAY-1999; 99US-0136392.

28-MAY-1999; 99US-0136782.

01-JUN-1999; 99US-0137222.

03-JUN-1999; 99US-0137258.

04-JUN-1999; 99US-0137502.

07-JUN-1999; 99US-0137724.

08-JUN-1999; 99US-0138094.

10-JUN-1999; 99US-0138440.

10-JUN-1999; 99US-0138647.

14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 23-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145087.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145182.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147266.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 28-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 14-OCT-1999; 99US-0159584.
PR 18-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 67.6%; Score 14.2; DB 21; Length 61;
Best local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 19
DB 36 AGATTCTAGGAACACAAA 54

```

RESULT 33
AAT86363/c
ID AAT86363 standard; DNA; 81 BP.
XX
AC AAT86363;
XX
DT 27-APR-1998 (first entry)
XX
DE C. krusei non-transcribed intergene region-derived probe F-beta.
XX
KW Non-transcribed intergene region; IGR; ribosome; cistron; 25S; 18S;
KW probe; hybridisation; detection; differentiation; yeast; diagnosis;
KW Geotrichum candidum, ss.
XX
OS Synthetic.
OS Candida krusei.
XX
XX Key Location/Qualifiers
FH repeat_region 2..80
FT repeat_region /*tag= a
FH repeat_unit 2..7
FH repeat_unit /*tag= b
XX
XX WC9736003-At.
XX
XX 02-OCT-1997.
XX
XX 24-MAR-1997; 97WO-FR00518.
XX
XX 22-MAR-1996; 96FR-0003835.
XX
XX (INMR ) BIO MERIEUX.
XX
XX PA Carlotti A, Villard J;
XX
XX PI WPI; 1997-489661/45.
XX
XX DR
XX
XX PT Probe for detection and characterisation of yeast for diagnosis and
PT process control - comprises fragment derived from ribosomal DNA in
PT the non-transcribed intergene region that contains repeated
PT subsequences
XX
XX PS Claim 7; Page 30; 49pp; French.
XX
XX CC This is the sequence of probe F-alpha derived from the sequence of the
CC non-transcribed intergene region (IGR) F1 from Candida krusei
CC (AAT86363). The sequence is derived from a ribosomal cistron located in
CC the region between the 25S and 18S ribosomal DNA genes. Probes (see
CC AAT86362-T86365) derived from the IGR can be used for specific and/or
CC intraspecific detection, identification and/or differentiation of yeast
CC for medical diagnosis or for monitoring industrial processes,
CC specifically for Candida krusei and Geotrichum candidum.
XX
XX SQ Sequence 81 BP; 20 A; 5 C; 8 G; 48 T; 0 other;
XX
Query Match 67.6%; Score 14.2; DB 18; Length 81;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AGATTCTAGGAATTCAA 19
Db 65 AGATTCAAAAATTCAA 47
XX
RESULT 34
ABN41529/c
ID ABN41529 standard; DNA; 60 BP.
XX
AC ABN41529;
XX
XX 15-JUL-2002 (first entry)
XX

```

```

DE Human spliced transcript detection oligonucleotide SEQ ID NO:14277.
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
XX WO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 20-JUL-2001; 2001WO-IB01903.
XX
XX PR 28-JUL-2000; 2000US-221607P.
XX
XX PR 02-MAY-2001; 2001US-287724P.
XX
XX PA (COMP-) COMPUGEN INC.
XX
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX DR WPI; 2002-257383/30.
XX
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX PT selectively hybridize to mRNAs transcribed from a transcription unit of
XX PT a genome, useful for detecting tissue-, pathology-, and
XX PT developmental-specific genes
XX
XX PS Example 1; SEQ ID 14277; 47pp; English.
XX
XX CC The present invention describes oligonucleotide libraries for detecting
XX CC messenger RNAs that populate a (sub-)transcriptome, where the
XX CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX CC transcription units that populate a genome. The library comprises
XX CC several oligonucleotides, each capable of hybridising selectively to a
XX CC set of messenger RNAs transcribed from a given transcription unit of
XX CC the genome, which encodes one or more messenger RNA splice variants.
XX CC The oligonucleotide libraries are useful for detecting mRNAs from a
XX CC biological sample, in expression profiling studies, in qualitatively or
XX CC quantitatively characterising the corresponding transcriptome, and in
XX CC detecting RNA transcripts and splice variants of human or animal
XX CC transcriptomes. The libraries may also be used as specialised mini
XX CC libraries to detect transcripts of a sub-transcriptome under a
XX CC particular biological or pathological state, and so allowing the
XX CC detection of tissue- and pathology-specific genes such as those genes
XX CC only expressed in specific tissue under a specific pathological
XX CC condition; to detect developmental specific genes; and to detect RNA
XX CC transcripts and splice variants of a transcriptome of a patient suffering
XX CC from a particular disorder. ABN27253 to ABN59589 represent
XX CC oligonucleotide sequences from rats, humans and mice, which are used in
XX CC the exemplification of the present invention.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pat_sequences.
XX
XX SQ Sequence 60 BP; 17 A; 12 C; 15 G; 16 T; 0 other;
XX
Query Match 66.7%; Score 14; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GATTCTAGGAATT 15
Db 52 GATTCTAGGAATT 39
XX
RESULT 35
AAT58221/c
ID AAT58221 standard; DNA; 30 BP.
XX
AC AAT58221;
XX
XX 20-MAY-1997 (first entry)
XX

```

DE	Candida CYB1 gene primer.
XX	
KW	TYPI; CKS1; CDK1; CYB1; MOC1; CKM1; cell-cycle regulatory protein;
KW	Candida; anti-mycotic; antifungal; preservative; yeast;
XX	cyclin; kinase; phosphatase; ss.
OS	Synthetic.
XX	
FN	WO9639527-A1.
XX	
PD	12-DEC-1996.
XX	
FE	05-JUN-1996; 96WO-US08807.
XX	
PR	05-JUN-1995; 95US-0463090.
XX	
PA	(MITO-) MITOTIX INC.
FI	Cottarel G, Damagnez V, Draetta G;
XX	
DR	WPI; 1997-043149/04.
XX	
PT	New cell-cycle regulatory proteins from Candida - useful
PT	as anti-mycotic agents, as a preservative or in reagents and assays.
XX	
PS	Example 7; Page 37; 70pp; English.
XX	
CC	Six Candida genes have been isolated, which encode an apparent
CC	CDG5 phosphatase (TYPI), a p3suc1 homolog (CKS1), a cyclin
CC	dependent kinase (CDK1), a cyclin (CYB1), a CDK-activating kinase
CC	catalytic subunit (MOC1), and a Map kinase (CKM1) (AAT6446 to
CC	AAT6451). The TYPI polypeptide and nucleic acid is claimed, where
CC	TYPI is at least 75% homologous to the amino acid sequence given
CC	in Seg 2, according to the claims of the specification. According
CC	to the disclosure, Seg 2 encodes CKS1 (AAT6446) and Seg 1 encodes
CC	TYPI (AAT6447).
CC	The products may be used in reagents and assays which permit the
CC	rapid detection and evaluation of Candida yeast infections and for
CC	identifying opds. which have antifungal properties and which may be
CC	used as anti-mycotic agents. Such agents can be used therapeutically,
CC	as well as, for example, preservatives in foodstuff, feed supplement
CC	for promoting weight gain in livestock, or in disinfectant
CC	formulations for treatment of non-living matter, e.g. for
CC	decontaminating hospital equipment and rooms.
XX	
SC	Sequence 30 BP; 10 A; 6 C; 4 G; 10 T; 0 other;
XX	
QY	Query Match 65.7%; Score 13.8; DB 18; Length 30;
	Best Local Similarity 88.2%; Pred. No. 6.1e+03;
DB	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	3 ATTTCAGGAATTCAA 19
	20 ATTAAGAATTCAA 4
RESULT 36	
ID	AAV04870/c
AC	AAV04870 standard; DNA; 30 BP.
DT	AAV04870;
DT	30-APR-1998 (first entry)
DE	PCR primer 2 used to amplify the PTPase domain of GLEP1.
KW	Glomerular epithelial protein 1; GLEP1; podocyte; gene therapy;
KW	fibronectin type III-like repeat; protein tyrosine phosphatase domain;
KW	PTPase domain; glomerular disorder; low level; GLEP1 expression;
XX	PCR primer; ss.
OS	Synthetic.
XX	

PN	US5705623-A.
XX	
PD	06-JAN-1998.
XX	
FF	25-FEB-1994; 94US-0201697.
XX	
PR	25-FEB-1994; 94US-0201697.
XX	
PA	(UNMI) UNIV MICHIGAN.
XX	
F1	Thomas PE, Wiggins RC;
XX	
DR	WPI, 1998-086195/08.
XX	
PT	DNA encoding glomerular epithelial protein 1 - useful for gene therapy of glomerular disorders
XX	
PS	Example 3; Column 14; 47pp; English.
XX	
CC	PCR primers AAV04869-70 were used to amplify the glomerular epithelial protein 1 (GLEPPI) protein tyrosine phosphatase (PTPase) segment.
CC	The PCR product was cloned to produce a fusion protein, which was tested to confirm that the PTPase domain of GLEPPI had PTPase activity.
CC	The GLEPPI protein is primarily expressed in mammalian podocytes.
CC	The protein has a large extracellular domain with a sequence containing 8 fibronectin type III-like repeats, a hydrophobic transmembrane segment and a single intracellular protein tyrosine phosphatase (PTPase) domain.
CC	The GLEPPI nucleic acids are used for gene therapy of glomerular disorders associated with abnormally low levels of GLEPPI expression.
XX	
SQ	Sequence 30 BP; 7 A; 6 C; 4 G; 13 T; 0 other;
OY	Query Match 65.7%; Score 13.8; DB 19; Length 30; Best Local Similarity 88.2%; Pred. No. 6.1e+03; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
Db	3 ATTCTAGCAATTCAAA 19 17 AGTCTAGCAATTCAAA 1
RESULT 37	
AZ08279/C	
ID	AAZ08279 standard; DNA; 30 BP.
XX	
AC	AAZ08279;
XX	
DT	07-FEB-2000 (First entry)
XX	
DE	PCR primer-1 used for amplification of Candida CYB1 gene.
XX	
KW	Cell cycle regulatory protein; CYB1 gene; Candida; coding sequence; Kw EcoRI; restriction site; primer; amplify; subclone; pUG4-5 vector; KW CYB1-Vp16 fusion protein; ss.
XX	
OS	Synthetic.
XX	
FN	WO9957536-A2.
XX	
PD	11-NOV-1999.
XX	
PF	05-MAY-1999; 99WO-US09878.
XX	
PR	05-MAY-1998; 98US-0072994.
XX	
PA	(MITO-) MITOTIX INC.
XX	
PI	Berlin V, Cottarel G, Damagnez V, Rudolph J, Sullivan D;
XX	
DR	WPI, 2000-03847/03.
XX	
PT	New Candida cyclin activated kinase 1, useful for generating vaccines and screening for its inhibitors -
PT	

XX Example 7; Page 60; 109pp; English.
 PS
 CC The present DNA sequence is the PCR primer-1, that has the EcoRI
 CC restriction site. It is used to amplify the Candida CYP1 coding sequence
 CC and is subcloned into pUG4-5 vector to create a CYP1-VPL6 fusion protein.
 XX
 SQ Sequence 30 BP; 10 A; 6 C; 4 G; 10 T; 0 other;
 QY
 Db 3 ATTTAGGAATTCAA 19
 20 ATTACTATGAATTCAA 4
 RESULT 38
 ABN47639
 ID ABN47639 standard; DNA; 60 BP.
 AC
 XX ABN47639;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:20387.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 EN
 PD 07-FEB-2002.
 XX
 PE 20-JUL-2001; 2001WO-IB01903.
 XX
 PR 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes
 XX
 PS Example 1; SEQ ID 20387; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering

CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 60 BP; 13 A; 8 C; 21 G; 18 T; 0 other;
 QY
 Db 1 AGATTCTAGGAATTCA 17
 33 AGCTTCTCGGAATTCA 49
 RESULT 39
 ABN57384/C
 ID ABN57384 standard; DNA; 65 BP.
 AC
 XX ABN57384;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:30132.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200210449-A2.
 EN
 PD 07-FEB-2002.
 XX
 PE 20-JUL-2001; 2001WO-IB01903.
 XX
 PR 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes
 XX
 PS Example 1; SEQ ID 30132; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridizing selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering

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CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 65 BP; 22 A; 19 C; 11 G; 13 T; 0 other;

Query Match 65.7%; Score 13.8; DB 24; Length 65;
Best Local Similarity 88.2%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TTCTAGGAAATTCGAATC 21
Db 62 TTCTAGGAAATTCGAATC 46

RESULT 40
AAQ32872/c
ID AAQ32872 standard; DNA; 22 BP.

XX
AC AAQ32872;

XX
DT 29-APR-1993 (first entry)

XX
DE Human apolipoprotein exon 4 plus-strand primer #2.

XX
KW anchored polymerase chain reaction; APCR; apoE; mismatch;

XX
KM epsilon 2; epsilon 4; epsilon 5; epsilon 7; ss.

XX
OS Synthetic.

XX
PN JP04320700-A.

XX
PD 11-NOV-1992.

XX
PE 17-APR-1991; 91JP-0112435.

XX
PR 17-APR-1991; 91JP-0112435.

XX
PA (NNTN) NIPPON SHUJI KK.

XX
DR WPI; 1992-426692/52.

XX
PT Testing apolipoprotein E genotype - using polymerase chain
PT reaction primers and labelled allele-specific oligonucleotide
PT probe for hybridisation to amplified deoxyribonucleic acid

XX
PS Claim 4; Page 11; 16pp; Japanese.

XX
CC Primer #2 corresponds to nucleotides 5'-3618-3639-3' of ApoE. This
CC plus-strand primer is used with minus strand primer #4

XX
CC (3'-4220-4241-5', see AAQ32874) to amplify exon 4 of the human
CC apolipoprotein gene. The epsilon 2, 4 and 7 mismatch mutations occur
CC in this region, at positions 3883, 3745 and 4141 and 4144,

XX
CC respectively. Three sets of four oligonucleotide probes were prepared
CC to distinguish the wild-type from the mutant base at the mismatch

XX
CC position for both the plus and the minus strands. The probe sets
CC are AAQ32875-6 and AAQ32883-4 for epsilon 2, AAQ32877-8 and AAQ32885-6

XX
CC for epsilon 4 and AAQ32881-2 and AAQ32889-90 for epsilon 7.

XX
SQ Sequence 22 BP; 7 A; 4 C; 7 G; 4 T; 0 other;

Query Match 64.8%; Score 13.6; DB 13; Length 22;
Best Local Similarity 80.0%; Pred. No. 7.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GATTCTAGGAAATTCGAATC 21
Db 21 GATTCTAGGAAATTCGAATC 2

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OM nucleic - nucleic search, using sw model

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Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	85.7	21 11	US-09-877-705A-91
3	18	85.7	21 11	US-09-877-705A-92
4	18	85.7	21 11	US-09-877-738A-91
5	18	85.7	21 11	US-09-877-738A-92
6	18	85.7	63 11	US-09-877-705A-154
7	18	85.7	63 11	US-09-877-738A-154
8	18	85.7	100 10	US-09-923-246-59
9	18	85.7	100 10	US-09-923-246-60
10	18	85.7	100 10	US-09-825-561A-48
11	18	85.7	100 10	US-09-825-561A-49
12	18	85.7	100 11	US-09-892-949-43
13	18	85.7	100 11	US-09-892-949-44
14	18	85.7	100 13	US-10-282-622-17
15	18	85.7	100 13	US-10-282-622-18

16	18	85.7	100 13	US-10-351-157-44	Sequence 44, Appl
17	18	85.7	100 13	US-10-351-157-45	Sequence 45, Appl
18	18	85.7	100 13	US-10-295-723-59	Sequence 59, Appl
19	18	85.7	100 15	US-10-295-723-60	Sequence 60, Appl
20	15.4	73.3	24 13	US-10-325-606-1	Sequence 1, Appl
21	14.8	70.5	41 12	US-10-327-481A-21	Sequence 21, Appl
22	14.8	70.5	41 12	US-10-327-481A-23	Sequence 23, Appl
23	14.8	70.5	44 12	US-10-327-481A-19	Sequence 19, Appl
24	14.8	70.5	44 12	US-10-327-481A-25	Sequence 25, Appl
25	14.6	69.5	58 12	US-09-932-679-42	Sequence 42, Appl
26	14.6	69.5	58 13	US-09-932-679-43	Sequence 43, Appl
27	14.2	67.6	99 10	US-09-969-373-1158	Sequence 1158, Ap
28	14.2	66.7	60 13	US-09-908-975-14277	Sequence 14277, A
29	13.8	65.7	20 11	US-09-920-073-115	Sequence 115, App
30	13.8	65.7	20 12	US-10-388-263-651	Sequence 651, App
31	13.8	65.7	20 13	US-10-147-156-115	Sequence 115, App
32	13.8	65.7	60 13	US-09-908-975-20387	Sequence 20387, A
33	13.8	65.7	65 13	US-09-908-975-30132	Sequence 30132, A
34	13.6	64.8	25 15	US-10-098-263B-26232	Sequence 26232, A
35	13.6	64.8	44 13	US-10-307-441-42	Sequence 42, Appl
36	13.4	63.8	28 12	US-09-927-876-69	Sequence 69, Appl
37	13.4	63.8	28 13	US-10-360-149-69	Sequence 69, Appl
38	13.4	63.8	65 13	US-09-908-975-28326	Sequence 28326, A
39	13.2	62.9	19 13	US-10-251-117-633	Sequence 633, App
40	13.2	62.9	19 13	US-10-251-117-940	Sequence 940, App
41	13.2	62.9	25 15	US-10-098-263B-107625	Sequence 107625, A
42	13.2	62.9	42 13	US-10-154-460-2	Sequence 2, Appl
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46	13.2	62.9	60 13	US-09-737-476B-39	Sequence 39, Appl
47	13.2	62.9	63 13	US-10-197-293-38	Sequence 38, Appl
48	13.2	62.9	65 13	US-10-032-585-2560	Sequence 2560, Ap
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50	13	61.9	23 11	US-09-828-344-12	Sequence 12, Appl
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63	13	61.9	35 13	US-10-364-276-2	Sequence 2, Appl
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66	13	61.9	50 10	US-09-832-659-30	Sequence 30, Appl
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C	103	12.6	60.0	37	13	US-10-317-250-10	Sequence 10, Appl	176	12.2	58.1	24	11	US-09-997-573-190	Sequence 190, App
C	104	12.6	60.0	39	13	US-10-005-956-1360	Sequence 1360, Ap	177	12.2	58.1	24	11	US-09-991-172-190	Sequence 190, App
C	105	12.6	60.0	39	15	US-10-005-956-1494	Sequence 1494, Ap	178	12.2	58.1	24	11	US-09-990-726-190	Sequence 190, App
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C	135	12.4	59.0	50	12	US-10-131-827-3852	Sequence 2852, App	208	12.2	58.1	24	13	US-10-219-538-190	Sequence 190, App
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C	149	12.2	58.1	24	10	US-09-991-073-190	Sequence 190, App	222	12.2	58.1	30	13	US-10-104-019-99	Sequence 99, Appl
C	150	12.2	58.1	24	10	US-09-990-442-190	Sequence 190, App	223	12.2	58.1	30	13	US-10-428-826-51	Sequence 51, Appl
C	151	12.2	58.1	24	10	US-09-991-163-190	Sequence 190, App	224	12.2	58.1	30	14	US-10-104-019-99	Sequence 99, Appl
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C	154	12.2	58.1	24	10	US-09-989-721-190	Sequence 190, App	227	12.2	58.1	43	15	US-10-001-886B-3	Sequence 3, Appl
C	155	12.2	58.1	24	10	US-09-992-598-190	Sequence 190, App	228	12.2	58.1	47	13	US-10-367-438-54	Sequence 54, Appl
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C	157	12.2	58.1	24	10	US-09-989-735-190	Sequence 190, App	230	12.2	58.1	52	9	US-10-287-519-451	Sequence 451, Appl
C	158	12.2	58.1	24	10	US-09-990-444-190	Sequence 190, App	231	12.2	58.1	52	9	US-09-777-564A-1717	Sequence 1717, Ap
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C 272	12	57.1	30	13	US-10-002-244-29	Sequence 29, Appli	C 345	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 273	12	57.1	30	13	US-10-246-229-6	Sequence 6, Appli	C 346	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 274	12	57.1	30	13	US-10-341-967-59	Sequence 29, Appli	C 347	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 275	12	57.1	30	15	US-10-044-967-5	Sequence 5, Appli	C 348	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 276	12	57.1	31	9	US-09-841-133-216	Sequence 216, App	C 349	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 277	12	57.1	31	11	US-09-848-616-9	Sequence 9, Appli	C 350	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 278	12	57.1	31	13	US-10-050-902-9	Sequence 9, Appli	C 351	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 279	12	57.1	31	13	US-10-050-902-9	Sequence 9, Appli	C 352	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 280	12	57.1	33	12	US-10-387-384-22	Sequence 22, Appli	C 353	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 281	12	57.1	33	13	US-09-731-030A-7	Sequence 7, Appli	C 354	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 282	12	57.1	37	10	US-10-327-592-4	Sequence 4, Appli	C 355	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 283	12	57.1	37	10	US-09-944-411-11	Sequence 11, Appli	C 356	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 284	12	57.1	38	10	US-09-759-352-1	Sequence 1, Appli	C 357	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 285	12	57.1	38	13	US-10-260-516-11	Sequence 11, Appli	C 358	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 286	12	57.1	39	13	US-10-220-612-9	Sequence 9, Appli	C 359	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 287	12	57.1	39	13	US-09-826-509-20	Sequence 20, Appli	C 360	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 288	12	57.1	43	13	US-10-032-585-841	Sequence 841, App	C 361	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 289	12	57.1	50	12	US-10-131-827-734	Sequence 734, App	C 362	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 290	12	57.1	50	12	US-10-131-827-5080	Sequence 5080, App	C 363	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 291	12	57.1	50	12	US-10-131-827-5919	Sequence 5919, App	C 364	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 292	12	57.1	50	12	US-10-131-827-7651	Sequence 7651, App	C 365	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 293	12	57.1	51	10	US-09-828-995B-91	Sequence 91, Appli	C 366	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 294	12	57.1	53	13	US-10-027-632-58675	Sequence 58675, A	C 367	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 295	12	57.1	53	14	US-10-027-632-58675	Sequence 58675, A	C 368	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 296	12	57.1	60	11	US-09-852-385-7	Sequence 7, Appli	C 369	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 297	12	57.1	60	13	US-09-908-975-6825	Sequence 6825, App	C 370	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 298	12	57.1	60	13	US-09-908-975-7405	Sequence 7405, App	C 371	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 299	12	57.1	60	13	US-09-908-975-8674	Sequence 8674, App	C 372	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 300	12	57.1	60	13	US-09-908-975-13716	Sequence 13716, A	C 373	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 301	12	57.1	60	13	US-09-908-975-14758	Sequence 14758, A	C 374	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 302	12	57.1	60	13	US-09-908-975-16941	Sequence 16941, A	C 375	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 303	12	57.1	60	13	US-09-908-975-19593	Sequence 19593, A	C 376	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 304	12	57.1	60	13	US-09-908-975-20092	Sequence 20092, A	C 377	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 305	12	57.1	60	13	US-09-908-975-20471	Sequence 20471, A	C 378	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 306	12	57.1	65	13	US-09-908-975-20471	Sequence 20471, A	C 379	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 307	12	57.1	65	13	US-09-908-975-3192	Sequence 3192, App	C 380	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A

C 381	11.8	56.2	50	11	US-09-904-786-79	Sequence 79, Appl	C 454	11.6	55.2	22	13	US-10-026-952-36	Sequence 36, Appl
C 382	11.8	56.2	50	11	US-09-906-646-79	Sequence 79, Appl	C 455	11.6	55.2	23	11	US-09-860-738C-8	Sequence 8, Appl
C 383	11.8	56.2	50	11	US-09-906-700-79	Sequence 79, Appl	C 456	11.6	55.2	23	11	US-10-291-171-16	Sequence 16, Appl
C 384	11.8	56.2	50	11	US-09-903-786-79	Sequence 79, Appl	C 457	11.6	55.2	23	15	US-10-081-980B-5	Sequence 5, Appl
C 385	11.8	56.2	50	11	US-09-902-903-79	Sequence 79, Appl	C 458	11.6	55.2	25	15	US-10-215-112-3087	Sequence 3087, Ap
C 386	11.8	56.2	50	11	US-09-903-749A-79	Sequence 79, Appl	C 459	11.6	55.2	25	15	US-10-215-112-3508	Sequence 3508, Ap
C 387	11.8	56.2	50	11	US-09-904-119-79	Sequence 79, Appl	C 460	11.6	55.2	25	15	US-10-098-263B-18794	Sequence 18794, A
C 388	11.8	56.2	50	11	US-09-904-936-79	Sequence 79, Appl	C 461	11.6	55.2	25	15	US-10-098-263B-40243	Sequence 40243, A
C 389	11.8	56.2	50	11	US-09-904-736-79	Sequence 79, Appl	C 462	11.6	55.2	25	15	US-10-098-263B-44235	Sequence 44235, A
C 390	11.8	56.2	50	11	US-09-907-794-79	Sequence 79, Appl	C 463	11.6	55.2	25	15	US-10-098-263B-46762	Sequence 46762, A
C 391	11.8	56.2	50	11	US-09-903-943-79	Sequence 79, Appl	C 464	11.6	55.2	25	15	US-10-098-263B-50109	Sequence 50109, A
C 392	11.8	56.2	50	11	US-09-904-462-79	Sequence 79, Appl	C 465	11.6	55.2	25	15	US-10-098-263B-68737	Sequence 68737, A
C 393	11.8	56.2	50	11	US-09-907-925-79	Sequence 79, Appl	C 466	11.6	55.2	25	15	US-10-098-263B-68738	Sequence 68738, A
C 394	11.8	56.2	50	11	US-09-902-692-79	Sequence 79, Appl	C 467	11.6	55.2	25	15	US-10-098-263B-87751	Sequence 86939, A
C 395	11.8	56.2	50	11	US-09-903-520-79	Sequence 79, Appl	C 468	11.6	55.2	25	15	US-10-098-263B-88593	Sequence 88593, A
C 396	11.8	56.2	50	11	US-09-905-056-79	Sequence 79, Appl	C 469	11.6	55.2	25	15	US-10-098-263B-99377	Sequence 99373, A
C 397	11.8	56.2	50	11	US-09-909-064-79	Sequence 79, Appl	C 470	11.6	55.2	25	15	US-10-098-263B-107626	Sequence 107626, A
C 398	11.8	56.2	50	11	US-09-904-553-79	Sequence 79, Appl	C 471	11.6	55.2	25	15	US-10-098-263B-125202	Sequence 125202, A
C 399	11.8	56.2	50	11	US-09-905-381-79	Sequence 79, Appl	C 472	11.6	55.2	25	15	US-10-098-263B-125838	Sequence 125838, A
C 400	11.8	56.2	50	11	US-09-905-088-79	Sequence 79, Appl	C 473	11.6	55.2	27	15	US-10-062-809-68	Sequence 68, Appl
C 401	11.8	56.2	50	11	US-09-907-575-79	Sequence 79, Appl	C 474	11.6	55.2	28	13	US-10-026-952-38	Sequence 38, Appl
C 402	11.8	56.2	50	11	US-09-905-075-79	Sequence 79, Appl	C 475	11.6	55.2	31	9	US-09-801-874-1015	Sequence 1015, Ap
C 403	11.8	56.2	50	11	US-09-902-759-79	Sequence 79, Appl	C 476	11.6	55.2	32	9	US-09-844-813-6	Sequence 6, Appl
C 404	11.8	56.2	50	11	US-09-902-634-79	Sequence 79, Appl	C 477	11.6	55.2	33	13	US-09-832-899-20	Sequence 20, Appl
C 405	11.8	56.2	50	11	US-09-902-713-79	Sequence 79, Appl	C 478	11.6	55.2	40	11	US-09-828-523A-52	Sequence 52, Appl
C 406	11.8	56.2	50	11	US-09-907-979-79	Sequence 79, Appl	C 479	11.6	55.2	40	11	US-09-966-521-92	Sequence 92, Appl
C 407	11.8	56.2	50	11	US-09-902-615-79	Sequence 79, Appl	C 480	11.6	55.2	40	13	US-10-429-094-92	Sequence 92, Appl
C 408	11.8	56.2	50	11	US-09-903-925-79	Sequence 79, Appl	C 481	11.6	55.2	42	15	US-10-091-135-54	Sequence 54, Appl
C 409	11.8	56.2	50	11	US-09-906-760A-79	Sequence 79, Appl	C 482	11.6	55.2	43	13	US-10-032-585-1712	Sequence 1712, Ap
C 410	11.8	56.2	50	11	US-09-903-823-79	Sequence 79, Appl	C 483	11.6	55.2	44	12	US-09-775-925-19	Sequence 19, Appl
C 411	11.8	56.2	50	11	US-09-907-652-79	Sequence 79, Appl	C 484	11.6	55.2	47	12	US-10-349-143-690	Sequence 690, App
C 412	11.8	56.2	50	11	US-09-902-572A-79	Sequence 79, Appl	C 485	11.6	55.2	47	12	US-10-349-143-1489	Sequence 1489, App
C 413	11.8	56.2	50	11	US-09-902-979-79	Sequence 79, Appl	C 486	11.6	55.2	47	12	US-10-349-143-1713	Sequence 1713, Ap
C 414	11.8	56.2	50	11	US-09-905-125-79	Sequence 79, Appl	C 487	11.6	55.2	47	12	US-10-349-143-1713	Sequence 3713, Ap
C 415	11.8	56.2	50	11	US-09-906-815A-79	Sequence 79, Appl	C 488	11.6	55.2	49	15	US-10-291-230-5	Sequence 5, Appl
C 416	11.8	56.2	50	12	US-09-908-576-79	Sequence 79, Appl	C 489	11.6	55.2	49	15	US-10-291-249-5	Sequence 995, App
C 417	11.8	56.2	50	12	US-10-448-713-79	Sequence 79, Appl	C 490	11.6	55.2	50	12	US-10-131-827-995	Sequence 1066, App
C 418	11.8	56.2	50	12	US-10-449-656-79	Sequence 79, Appl	C 491	11.6	55.2	50	12	US-10-131-827-1067	Sequence 1067, Ap
C 419	11.8	56.2	50	12	US-10-131-827-636	Sequence 636, App	C 492	11.6	55.2	50	12	US-10-131-827-1067	Sequence 1067, Ap
C 420	11.8	56.2	50	12	US-10-131-827-8091	Sequence 8091, Ap	C 493	11.6	55.2	50	12	US-10-131-827-1067	Sequence 1067, Ap
C 421	11.8	56.2	50	13	US-09-903-806-79	Sequence 79, Appl	C 494	11.6	55.2	50	12	US-10-131-827-7850	Sequence 7850, Ap
C 422	11.8	56.2	50	13	US-09-905-449-79	Sequence 79, Appl	C 495	11.6	55.2	52	15	US-10-062-809-60	Sequence 60, Appl
C 423	11.8	56.2	50	13	US-09-904-992-79	Sequence 79, Appl	C 496	11.6	55.2	60	13	US-09-908-975-7489	Sequence 7489, Ap
C 424	11.8	56.2	50	13	US-09-903-603A-79	Sequence 79, Appl	C 497	11.6	55.2	60	13	US-09-908-975-9568	Sequence 9568, Ap
C 425	11.8	56.2	50	13	US-09-904-838-79	Sequence 79, Appl	C 498	11.6	55.2	60	13	US-09-908-975-12289	Sequence 12289, A
C 426	11.8	56.2	50	13	US-09-906-777-79	Sequence 79, Appl	C 499	11.6	55.2	60	13	US-09-908-975-13415	Sequence 13415, A
C 427	11.8	56.2	50	13	US-09-904-532-79	Sequence 79, Appl	C 500	11.6	55.2	60	13	US-09-908-975-14262	Sequence 14262, A
C 428	11.8	56.2	50	13	US-09-904-766-79	Sequence 79, Appl	C 501	11.6	55.2	60	13	US-09-908-975-17086	Sequence 17086, A
C 429	11.8	56.2	50	13	US-09-904-920A-79	Sequence 79, Appl	C 502	11.6	55.2	60	13	US-09-908-975-20914	Sequence 20914, A
C 430	11.8	56.2	50	13	US-10-299-976-79	Sequence 79, Appl	C 503	11.6	55.2	60	13	US-09-908-975-21728	Sequence 21728, A
C 431	11.8	56.2	50	13	US-09-903-562-79	Sequence 79, Appl	C 504	11.6	55.2	64	11	US-09-950-920-8	Sequence 8, Appl
C 432	11.8	56.2	50	13	US-09-904-877A-79	Sequence 79, Appl	C 505	11.6	55.2	64	11	US-10-027-632-58365	Sequence 58365, A
C 433	11.8	56.2	50	13	US-10-299-937-79	Sequence 79, Appl	C 506	11.6	55.2	64	14	US-10-027-632-58365	Sequence 58365, A
C 434	11.8	56.2	50	13	US-09-906-618-79	Sequence 79, Appl	C 507	11.6	55.2	65	13	US-09-908-975-1594	Sequence 1594, Ap
C 435	11.8	56.2	50	13	US-09-907-128-79	Sequence 79, Appl	C 508	11.6	55.2	65	13	US-09-908-975-3090	Sequence 3090, Ap
C 436	11.8	56.2	50	13	US-09-904-805-79	Sequence 79, Appl	C 509	11.6	55.2	65	13	US-09-908-975-26477	Sequence 26477, A
C 437	11.8	56.2	50	13	US-09-904-938A-79	Sequence 79, Appl	C 510	11.6	55.2	65	13	US-09-908-975-28020	Sequence 28020, A
C 438	11.8	56.2	50	13	US-09-906-722A-79	Sequence 79, Appl	C 511	11.6	55.2	65	13	US-10-032-585-315	Sequence 315, App
C 439	11.8	56.2	55	9	US-09-860-996-23	Sequence 23, Appl	C 512	11.6	55.2	65	13	US-10-032-585-2565	Sequence 2565, Ap
C 440	11.8	56.2	60	10	US-09-832-659-9	Sequence 9, Appl	C 513	11.6	55.2	65	13	US-10-032-585-2793	Sequence 2793, Ap
C 441	11.8	56.2	60	11	US-09-832-658-3	Sequence 3, Appl	C 514	11.6	55.2	65	13	US-10-032-585-3018	Sequence 3018, Ap
C 442	11.8	56.2	60	11	US-09-908-975-5855	Sequence 5855, Ap	C 515	11.6	55.2	66	10	US-09-854-999-45	Sequence 45, Appl
C 443	11.8	56.2	60	13	US-09-908-975-15921	Sequence 15921, A	C 516	11.6	55.2	68	11	US-09-866-925-246	Sequence 246, App
C 444	11.8	56.2	60	13	US-09-908-975-18456	Sequence 18456, A	C 517	11.6	55.2	69	11	US-09-951-061A-4	Sequence 4, Appl
C 445	11.8	56.2	64	9	US-09-923-876-3468	Sequence 3468, Ap	C 518	11.6	55.2	69	11	US-10-267-884-4	Sequence 4, Appl
C 446	11.8	56.2	64	12	US-09-923-876-3468	Sequence 3468, Ap	C 519	11.6	55.2	72	13	US-10-159-006-72	Sequence 72, Appl
C 447	11.8	56.2	65	13	US-09-908-975-24580	Sequence 24580, A	C 520	11.6	55.2	72	13	US-10-159-006-72	Sequence 72, Appl
C 448	11.8	56.2	65	13	US-09-908-975-24580	Sequence 24580, A	C 521	11.6	55.2	74	14	US-10-027-632-176001	Sequence 176001, A
C 449	11.8	56.2	65	14	US-09-908-975-29552	Sequence 29552, A	C 522	11.6	55.2	74	14	US-10-027-632-176001	Sequence 176001, A
C 450	11.8	56.2	65	14	US-10-021-758-17	Sequence 17, Appl	C 523	11.6	55.2	75	9	US-09-864-761-28074	Sequence 28074, A
C 451	11.8	56.2	83	10	US-09-783-590-9721	Sequence 9721, Ap	C 524	11.6	55.2	78	8	US-08-781-986A-4894	Sequence 4894, A
C 452	11.8	56.2	90	10	US-09-867-701-1274	Sequence 1274, Ap	C 525	11.6	55.2	79	9	US-09-864-761-19195	Sequence 19195, A
C 453	11.6	55.2	20	9	US-09-802-669-174	Sequence 174, Ap	C 526	11.6	55.2	79	9	US-09-864-761-19195	Sequence 19195, A

527	11.6	55.2	79	9	US-09-864-761-19717	Sequence 19717, A	600	11.4	54.3	50	10	US-09-999-832A-521	Sequence 521, App
528	11.6	55.2	81	13	US-10-029-386-22106	Sequence 22106, A	601	11.4	54.3	50	11	US-09-978-189-521	Sequence 521, App
529	11.6	55.2	82	9	US-09-864-761-26051	Sequence 26051, A	602	11.4	54.3	50	11	US-09-924-366A-7	Sequence 7, Appli
530	11.6	55.2	87	11	US-09-213-932A-4	Sequence 4, Appli	603	11.4	54.3	50	11	US-09-924-366A-10	Sequence 10, Appli
531	11.6	55.2	100	12	US-10-242-535A-54256	Sequence 54256, A	604	11.4	54.3	50	11	US-09-978-608A-521	Sequence 521, App
532	11.6	55.2	100	12	US-10-242-535A-54450	Sequence 54450, A	605	11.4	54.3	50	11	US-09-978-608A-521	Sequence 521, App
533	11.4	54.3	15	13	US-10-440-850-849	Sequence 849, App	606	11.4	54.3	50	11	US-09-978-191A-521	Sequence 521, App
534	11.4	54.3	20	10	US-09-371-900-42	Sequence 42, Appli	607	11.4	54.3	50	11	US-09-978-403A-521	Sequence 521, App
535	11.4	54.3	20	10	US-09-924-417-6	Sequence 6, Appli	608	11.4	54.3	50	11	US-09-978-564A-521	Sequence 521, App
536	11.4	54.3	20	11	US-09-824-322B-352	Sequence 352, App	609	11.4	54.3	50	11	US-09-999-833A-521	Sequence 521, App
537	11.4	54.3	20	11	US-09-824-322B-356	Sequence 356, App	610	11.4	54.3	50	11	US-09-981-915A-521	Sequence 521, App
538	11.4	54.3	20	12	US-10-289-762-6760	Sequence 6760, App	611	11.4	54.3	50	11	US-09-978-827A-521	Sequence 521, App
539	11.4	54.3	20	13	US-10-186-950-42	Sequence 42, Appli	612	11.4	54.3	50	11	US-09-918-585A-521	Sequence 521, App
540	11.4	54.3	21	11	US-09-948-747-11	Sequence 11, Appli	613	11.4	54.3	50	11	US-09-978-423A-521	Sequence 521, App
541	11.4	54.3	21	11	US-10-300-699-20	Sequence 20, Appli	614	11.4	54.3	50	11	US-09-978-193A-521	Sequence 521, App
542	11.4	54.3	21	13	US-10-443-923-12	Sequence 12, Appli	615	11.4	54.3	50	11	US-09-999-830A-521	Sequence 521, App
543	11.4	54.3	21	13	US-10-443-923-14	Sequence 14, Appli	616	11.4	54.3	50	11	US-09-978-707A-521	Sequence 521, App
544	11.4	54.3	22	9	US-09-874-626-5	Sequence 5, Appli	617	11.4	54.3	50	11	US-09-978-187B-521	Sequence 521, App
545	11.4	54.3	22	9	US-09-874-626-6	Sequence 6, Appli	618	11.4	54.3	50	11	US-09-978-643A-521	Sequence 521, App
546	11.4	54.3	22	11	US-09-948-747-12	Sequence 12, Appli	619	11.4	54.3	50	12	US-10-013-919A-521	Sequence 521, App
547	11.4	54.3	22	11	US-10-407-822-1	Sequence 4, Appli	620	11.4	54.3	50	12	US-10-013-920A-521	Sequence 521, App
548	11.4	54.3	23	12	US-10-384-974-47	Sequence 47, Appli	621	11.4	54.3	50	12	US-10-145-093A-521	Sequence 521, App
549	11.4	54.3	23	13	US-09-998-966-48	Sequence 48, Appli	622	11.4	54.3	50	12	US-10-131-827-497	Sequence 497, App
550	11.4	54.3	23	15	US-10-004-415-48	Sequence 44, Appli	623	11.4	54.3	50	12	US-10-131-827-953	Sequence 953, App
551	11.4	54.3	25	12	US-09-927-876-64	Sequence 64, Appli	624	11.4	54.3	50	12	US-10-131-827-2049	Sequence 2049, App
552	11.4	54.3	25	13	US-10-360-149-64	Sequence 64, Appli	625	11.4	54.3	50	12	US-10-131-827-2248	Sequence 2248, App
553	11.4	54.3	25	14	US-10-136-517-6	Sequence 6, Appli	626	11.4	54.3	50	12	US-10-131-827-3773	Sequence 3773, App
554	11.4	54.3	25	15	US-10-215-112-5840	Sequence 5840, App	627	11.4	54.3	50	12	US-10-131-827-3914	Sequence 3914, App
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556	11.4	54.3	25	15	US-10-098-263B-6678	Sequence 6678, App	629	11.4	54.3	50	12	US-10-131-827-4282	Sequence 4282, App
557	11.4	54.3	25	15	US-10-098-263B-8506	Sequence 8506, App	630	11.4	54.3	50	12	US-10-131-827-4471	Sequence 4471, App
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576	11.4	54.3	29	15	US-10-153-363A-42	Sequence 42, Appli	649	11.4	54.3	50	13	US-10-160-527A-521	Sequence 521, App
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588	11.4	54.3	43	13	US-10-032-585-885	Sequence 885, App	661	11.4	54.3	50	13	US-09-978-665A-521	Sequence 521, App
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595	11.4	54.3	47	12	US-10-343-143-1892	Sequence 1892, App	668	11.4	54.3	50	13	US-10-143-026B-521	Sequence 521, App
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683	11.4	54.3	60	13	US-09-908-975-5315	Sequence 5315, Ap	C 756	11.4	54.3	86	10	US-09-764-873-3	Sequence 3, Appli
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C 883	11.4	54.3	86	15	US-10-125-540-3	Sequence 3, Appli	C 956	11.2	53.3	26	10	US-10-098-263B-119742	Sequence 2, Appli
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C 886	11.4	54.3	86	15	US-10-144-929-3	Sequence 3, Appli	C 959	11.2	53.3	28	15	US-10-268-619-7	Sequence 7, Appli
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C 890	11.4	54.3	86	15	US-10-074-095-3	Sequence 3, Appli	C 963	11.2	53.3	30	13	US-10-071-867-67	Sequence 98, Appli
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C 967 11.2 53.3 30 15 US-10-263-250-3 Sequence 3, Appl
C 968 11.2 53.3 31 13 US-10-238-700-1864 Sequence 1864, Ap
C 969 11.2 53.3 32 9 US-09-314-477-28 Sequence 28, Appl
C 970 11.2 53.3 32 9 US-09-765-272-409 Sequence 409, App
C 971 11.2 53.3 33 8 US-08-929-464-4 Sequence 4, Appl
C 972 11.2 53.3 33 9 US-09-778-320-299 Sequence 299, App
C 973 11.2 53.3 33 9 US-09-910-689-299 Sequence 299, App
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C 975 11.2 53.3 34 12 US-10-371-877-31 Sequence 31, Appl
C 976 11.2 53.3 35 11 US-09-885-453-11 Sequence 11, Appl
C 977 11.2 53.3 35 15 US-10-079-384-47 Sequence 47, Appl
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C 980 11.2 53.3 37 13 US-10-161-547-35 Sequence 35, Appl
C 981 11.2 53.3 37 15 US-10-159-901-26 Sequence 26, Appl
C 982 11.2 53.3 38 9 US-09-765-272-415 Sequence 415, Appl
C 983 11.2 53.3 38 13 US-10-204-355-3 Sequence 3, Appl
C 984 11.2 53.3 39 12 US-10-371-877-30 Sequence 30, Appl
C 985 11.2 53.3 39 13 US-10-210-152-264 Sequence 264, App
C 986 11.2 53.3 39 14 US-10-135-322-38 Sequence 38, Appl
C 987 11.2 53.3 40 13 US-10-027-632-175486 Sequence 175486,
C 988 11.2 53.3 40 14 US-10-027-632-175486 Sequence 175486,
C 989 11.2 53.3 41 9 US-09-782-361-18 Sequence 18, Appl
C 990 11.2 53.3 42 13 US-09-996-008B-5 Sequence 18, Appl
C 991 11.2 53.3 43 13 US-10-032-585-1694 Sequence 1694, Ap
C 992 11.2 53.3 44 9 US-09-782-361-19 Sequence 19, Appl
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C 995 11.2 53.3 45 13 US-10-374-603-4 Sequence 4, Appl
C 996 11.2 53.3 47 12 US-10-349-143-2964 Sequence 2964, Ap
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C 998 11.2 53.3 47 12 US-10-455-013-8 Sequence 8, Appl
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ALIGNMENTS

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RESULT 1
US-09-954-987B-30
; Sequence 30, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; APPLICANT: Hermann Wagner
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AMS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-954-987B-30
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Query Match 85.7%; Score 18; DB 11; Length 20;

Best Local Similarity 100.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGATTCTAGGAATTCAA 18
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RESULT 2

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US-09-877-705A-91
; Sequence 91, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP91
US-09-877-705A-91
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Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGATTCTAGGAATTCAA 18
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RESULT 3

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US-09-877-705A-92/C
; Sequence 92, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP92
US-09-877-705A-92
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Query Match 85.7%; Score 18; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AGATTCTAGGAATTCAA 4
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RESULT 4

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US-09-877-738A-91
; Sequence 91, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
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; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP91
; US-09-877-738A-91

Query Match
; Sequence 92, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
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; SEQ ID NO 92
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP92
; US-09-877-738A-92

Query Match
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; Best Local Similarity 100.0%; Pred. No. 70;
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Db 1 AGATTCTAGGAATTCAA 18

RESULT 5
; US-09-877-738A-92/C
; Sequence 92, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
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; LENGTH: 21
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP92
; US-09-877-738A-92

Query Match
; Sequence 18, DB 11, Length 21,
; Best Local Similarity 100.0%; Pred. No. 70;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AGATTCTAGGAATTCAA 4

RESULT 6
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; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
; FILE OF INVENTION: FACTOR ACTIVITY
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
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; OTHER INFORMATION: Hybridization probe MP92
; US-09-877-705A-154

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RESULT 7
; US-09-877-738A-154/C
; Sequence 154, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
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; OTHER INFORMATION: Hybridization probe MP92
; US-09-877-738A-154

Query Match
; Sequence 18, DB 11, Length 63;
; Best Local Similarity 100.0%; Pred. No. 87;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
Db 63 AGATTCTAGGAATTCAA 46

RESULT 8
; US-09-923-246-59
; Sequence 59, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial sequence
```

```

; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC12749
US-09-923-246-59
Query Match      85.7%; Score 18; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
Db      67 AGATTCTAGGAATTCAA 84

RESULT 9
US-09-923-246-60/c
; Sequence 60, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC12748
US-09-923-246-60

Query Match      85.7%; Score 18; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
Db      38 AGATTCTAGGAATTCAA 21

RESULT 10
US-09-825-561A-48
; Sequence 48, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
```

```

; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12749
US-09-825-561A-48

Query Match      85.7%; Score 18; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
Db      67 AGATTCTAGGAATTCAA 84

RESULT 11
US-09-825-561A-49/c
; Sequence 49, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12748
US-09-825-561A-49

Query Match      85.7%; Score 18; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
Db      38 AGATTCTAGGAATTCAA 21

RESULT 12
US-09-892-949-43
; Sequence 43, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuitjper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
```



```
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12749
US-09-892-949-43
```

```
Query Match      85.7%; Score 18; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 AGATTCTAGGAATTCAA 18
        |||
Db      67 AGATTCTAGGAATTCAA 84
```

```
RESULT 13
US-09-892-949-44/c
; Sequence 44, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Maurer, Mark E.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12748
US-09-892-949-44
```

```
Query Match      85.7%; Score 18; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 AGATTCTAGGAATTCAA 18
        |||
Db      38 AGATTCTAGGAATTCAA 21
```

```
RESULT 14
US-10-282-622-17
; Sequence 17, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
```

```
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC12,749
US-10-282-622-17
```

```
Query Match      85.7%; Score 18; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 AGATTCTAGGAATTCAA 18
        |||
Db      67 AGATTCTAGGAATTCAA 84
```

```
RESULT 15
US-10-282-622-18/c
; Sequence 18, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC12,748
US-10-282-622-18
```

```
Query Match      85.7%; Score 18; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 AGATTCTAGGAATTCAA 18
        |||
Db      38 AGATTCTAGGAATTCAA 21
```

```
RESULT 16
US-10-351-157-44
; Sequence 44, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
```

APPLICANT: No. US20030215838A1ak, Julia E.
APPLICANT: Gross, Jane A.
APPLICANT: Dillon, Stacey R.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
FILE REFERENCE: 02-02
CURRENT APPLICATION NUMBER: US/10/351,157
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/435,361
PRIOR FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/389,108
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/350,325
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 183
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 100
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC12749
US-10-351-157-44

Query Match 85.7%; Score 18; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCNA 18
DB 67 AGATTCTAGGAATTCNA 84

RESULT 17
US-10-351-157-45/c
Sequence 45, Application US/10351157
Publication No. US20030215838A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Gao, Zeren
APPLICANT: Kalliper, Joseph L.
APPLICANT: Dasovich, Maria M.
APPLICANT: Grant, Francis J.
APPLICANT: Presnell, Scott R.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Hammond, Angela K.
APPLICANT: No. US20030215838A1ak, Julia E.
APPLICANT: Gross, Jane A.
APPLICANT: Dillon, Stacey R.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
FILE REFERENCE: 02-02
CURRENT APPLICATION NUMBER: US/10/351,157
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US 60/435,361
PRIOR FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/389,108
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/350,325
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 183
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 100
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC12748
US-10-351-157-45

Query Match 85.7%; Score 18; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCNA 18

DB 38 AGATTCTAGGAATTCNA 21

RESULT 18
US-10-295-723-59
Sequence 59, Application US/10295723
Publication No. US20030125524A1
GENERAL INFORMATION:
APPLICANT: No. US20030125524A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 100
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC12749
US-10-295-723-59

Query Match 85.7%; Score 18; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCNA 18
DB 67 AGATTCTAGGAATTCNA 84

RESULT 19
US-10-295-723-60/c
Sequence 60, Application US/10295723
Publication No. US20030125524A1
GENERAL INFORMATION:
APPLICANT: No. US20030125524A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 100
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC12748
US-10-295-723-60

Query Match 85.7%; Score 18; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
Db 38 AGATTCTAGGAATTCAA 21

RESULT 20
US-10-325-606-1/c
Sequence 1, Application US/10325606
Publication No. US20030216295A1
GENERAL INFORMATION:
APPLICANT: FUKUDA, MINORU
SAMADA, RITSUKO
TSUBOI, SHIGERU
TITLE OF INVENTION: E-SELECTIN-DEPENDENT CELL ADHESION
ANTAGONISTS

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE. 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,606
FILING DATE: 20-Dec-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/369,754
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1113

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-325-606-1

Query Match 73.3%; Score 15.4; DB 13; Length 24;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAA 19
Db 17 ATTCTAGGAATTCAA 1

RESULT 21
US-10-327-481A-21/c
Sequence 21, Application US/10327481A
Publication No. US20040001864A1
GENERAL INFORMATION:
APPLICANT: King, Andrew M.O.
APPLICANT: Burman, Allison J.
APPLICANT: Audonnet, Jean-Christophe F.
TITLE OF INVENTION: Vaccine against Foot-and-Mouth Disease
FILE REFERENCE: 454313-3178
CURRENT APPLICATION NUMBER: US/10/327,481A
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: PCT/FR01/02042
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: FR 0008437
PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 41
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: a fragment of about 3470 bp
US-10-327-481A-21

Query Match 70.5%; Score 14.8; DB 12; Length 41;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GATTCTAGGAATTCAA 19
Db 19 GATTCTAGGAATTCAA 2

RESULT 22
US-10-327-481A-23/c
Sequence 23, Application US/10327481A
Publication No. US20040001864A1
GENERAL INFORMATION:
APPLICANT: King, Andrew M.O.
APPLICANT: Burman, Allison J.
APPLICANT: Audonnet, Jean-Christophe F.

FILE REFERENCE: 454313-3178
TITLE OF INVENTION: Vaccine against Foot-and-Mouth Disease
CURRENT APPLICATION NUMBER: US/10/327,481A
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: PCT/FR01/02042
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: FR 0008437

PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23

LENGTH: 41
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: a fragment of about 3460 bp
US-10-327-481A-23

Query Match 70.5%; Score 14.8; DB 12; Length 41;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GATTTCTAGGAATTCAAA 19
Db 19 GATTTTATGAAATTCAAA 2

RESULT 23

US-10-327-481A-19/C
; Sequence 19, Application US/10327481A
; Publication No. US20040001864A1
; GENERAL INFORMATION:
; APPLICANT: King, Andrew M.O.
; APPLICANT: Burman, Alison J.
; APPLICANT: Audonnet, Jean-Christophe F.
; APPLICANT: Lombard, Michel F.A.
; TITLE OF INVENTION: Vaccine against Foot-and-Mouth Disease
; FILE REFERENCE: 454313-3178
; CURRENT APPLICATION NUMBER: US/10/327,481A
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/FR01/02042
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: FR 0008437
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: a oligonucleotide JCA323 used in PCR in example 6 to amplify
US-10-327-481A-19
Query Match 70.5%; Score 14.8; DB 12; Length 44;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GATTTCTAGGAATTCAAA 19
Db 19 GATTTTATGAAATTCAAA 2

RESULT 24

US-10-327-481A-25/C
; Sequence 25, Application US/10327481A
; Publication No. US20040001864A1
; GENERAL INFORMATION:
; APPLICANT: King, Andrew M.O.
; APPLICANT: Burman, Alison J.
; APPLICANT: Audonnet, Jean-Christophe F.
; APPLICANT: Lombard, Michel F.A.
; TITLE OF INVENTION: Vaccine against Foot-and-Mouth Disease
; FILE REFERENCE: 454313-3178
; CURRENT APPLICATION NUMBER: US/10/327,481A
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/FR01/02042
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: FR 0008437
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: a oligonucleotide JCA329 used in PCR in example 7 to amplify
US-10-327-481A-25
Query Match 70.5%; Score 14.8; DB 12; Length 44;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GATTTCTAGGAATTCAAA 19
Db 19 GATTTTATGAAATTCAAA 2

RESULT 25

US-09-932-679-42
; Sequence 42, Application US/09932679
; Patent No. US20020058801A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20020058801A1ak, Julia E.
; TITLE OF INVENTION: Mammalian Alpha Helical Protein-1
; FILE REFERENCE: 97-71D1
; CURRENT APPLICATION NUMBER: US/09/932,679
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/209,525
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/067,779
; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-932-679-42

Query Match 69.5%; Score 14.6; DB 9; Length 58;
Best Local Similarity 81.0%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AGATTTCTAGGAATTCAAATC 21
Db 14 AGAATACCTAGGAATTCCTACTC 34

RESULT 26

US-10-197-293-46
; Sequence 46, Application US/10197293
; Publication No. US20030171547A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49C1
; CURRENT APPLICATION NUMBER: US/10/197,293
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US 09/686,838
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/140,804
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/056,983
; PRIOR FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC14819
US-10-197-293-46

Query Match 69.5%; Score 14.6; DB 13; Length 58;
Best Local Similarity 81.0%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AGATTTCTAGGAATTCAAATC 21

Db 14 AGAATCTAGGAATCTATTC 34

RESULT 27

US-09-969-373-1158/c
; Sequence 1158, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Efferetz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SRS and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1158
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1158

Query Match 67.6%; Score 14.2; DB 10; Length 99;
Best Local Similarity 84.2%; Pred. No. 5.8e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATTCTTAGGAATTCATTC 21
Db 60 ATTATATGAAITGAAATC 42

RESULT 28

US-09-908-975-14277/c
; Sequence 14277, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Ilat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14277
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-14277

Query Match 66.7%; Score 14; DB 13; Length 60;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATTTCTAGGAATT 15
Db 52 GATTTCTAGGAATT 39

RESULT 29

US-09-920-033-115/c

; Sequence 115, Application US/09920033
; Publication No. US20030087853A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLOPROTEIN B EXPRESSION
; FILE REFERENCE: ISPH-0592
; CURRENT APPLICATION NUMBER: US/09/920,033
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 115
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-033-115

Query Match 65.7%; Score 13.8; DB 11; Length 20;
Best Local Similarity 88.2%; Pred. No. 6.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GATTTCTAGGAATCAA 18
Db 20 GATTTCAAGGATTCOA 4

RESULT 30

US-10-388-263-651/c
; Sequence 651, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowseert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmore, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSBQ for Windows Version 4.0
; SEQ ID NO 651
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-651

Query Match 65.7%; Score 13.8; DB 12; Length 20;
Best Local Similarity 88.2%; Pred. No. 6.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GATTTCTAGGAATCAA 18
Db 20 GATTTCAAGGATTCOA 4

RESULT 31

US-10-147-196-115/c
; Sequence 115, Application US/10147196
; Publication No. US20030215943A1
; GENERAL INFORMATION:

```

; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark U. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
; FILE REFERENCE: ISPH-0664
; CURRENT APPLICATION NUMBER: US/10/147,196
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 124
; SEQ ID NO 115
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-147-196-115

Query Match
Best Local Similarity 65.7%; Score 13.8; DB 13; Length 20;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GATTTCTAGGAATTCGA 18
Db 20 GATTTCAAGGAGATTCGA 4

RESULT 32
US-09-908-975-20387
; Sequence 20387, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20387
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-20387

Query Match
Best Local Similarity 65.7%; Score 13.8; DB 13; Length 60;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCGA 17
Db 33 AGCTTCTGGGAATTCGA 49

RESULT 33
US-09-908-975-30132/c
; Sequence 30132, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
```

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; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30132
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-30132

Query Match
Best Local Similarity 65.7%; Score 13.8; DB 13; Length 65;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TTCTAGGAATTCGAATC 21
Db 62 TTCTAGGAATTCGAGTC 46

RESULT 34
US-10-098-263B-26232/c
; Sequence 26232, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Maltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 26232
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-26232

Query Match
Best Local Similarity 64.8%; Score 13.6; DB 15; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCGAAT 20
Db 20 AGATATATAGTAATTCACAT 1

RESULT 35
US-10-307-441-42
; Sequence 42, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; TITLE OF INVENTION: Modified Research Council of Canada
; FILE REFERENCE: 027367-50060S
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 44
; TYPE: DNA
```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Tx-C1
US-10-307-441-42

Query Match 64.8%; Score 13.6; DB 13; Length 44;
Best Local Similarity 80.0%; Pred. No. 9.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GATTTAGGAATTCAAATC 21
Db 24 GATTTCTAGGAATTCGAAC 43

RESULT 36
US-09-927-876-69/c

Sequence 69, Application US/09927876
Publication No. US2004000554A1
GENERAL INFORMATION:
APPLICANT: El Tayar, Nabih
APPLICANT: Campbell, Robert K
APPLICANT: Kelton, Christie A
APPLICANT: He, Chaomei
TITLE OF INVENTION: No. US2004000554A1el Glycoproteins and Methods of Use Thereof
FILE REFERENCE: 20993-003
CURRENT APPLICATION NUMBER: US/09/927,876
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/225,035
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/202,724
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-927-876-69

Query Match 63.8%; Score 13.4; DB 12; Length 28;
Best Local Similarity 93.3%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTCTAGGAATTCAAA 19
Db 16 TACTAGGAATTCAAA 2

RESULT 37
US-10-360-149-69/c

Sequence 69, Application US/10360149
Publication No. US20030219786A1
GENERAL INFORMATION:
APPLICANT: El Tayar, Nabih
APPLICANT: Campbell, Robert K
APPLICANT: Kelton, Christie A
APPLICANT: He, Chaomei
TITLE OF INVENTION: No. US20030219786A1el Glycoproteins and Methods of Use Thereof
FILE REFERENCE: 20993-003
CURRENT APPLICATION NUMBER: US/10/360,149
CURRENT FILING DATE: 2003-02-06
PRIOR APPLICATION NUMBER: US/09/927,876
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/225,035
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/202,724
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69

LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-10-360-149-69

Query Match 63.8%; Score 13.4; DB 13; Length 28;
Best Local Similarity 93.3%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTCTAGGAATTCAAA 19
Db 16 TACTAGGAATTCAAA 2

RESULT 38
US-09-908-975-28326/c

Sequence 28326, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28326
LENGTH: 65
TYPE: DNA
ORGANISM: Mus musculus
US-09-908-975-28326

Query Match 63.8%; Score 13.4; DB 13; Length 65;
Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GATTTCTAGGAATTC 16
Db 58 GATTTCTAGGAATTC 44

RESULT 39
US-10-251-117-633/c

Sequence 633, Application US/10251117
Publication No. US20030170891A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSzigen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
FILE REFERENCE: 900/042 (MBHB02-468-A)
CURRENT APPLICATION NUMBER: US/10/251,117
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 10/163,552
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 09/916,466
PRIOR FILING DATE: 2001-07-25

```

; PRIOR APPLICATION NUMBER: US 60/296,243
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-251-117-633

Query Match      62.9%; Score 13.2; DB 13; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GATTCTAGAGAAATCAAA 19
        |||||
Db      19 GATTCTAGTCTCAAA 2

RESULT 40
US-10-251-117-940
; Sequence 940, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/042 (MBH802-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 940
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-251-117-940

Query Match      62.9%; Score 13.2; DB 13; Length 19;
Best Local Similarity 55.6%; Pred. No. 1.3e+04;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 GATTCTAGAGAAATCAAA 19
        |||||
Db      1 GAUUUCUAGGUUCUCAA 18

Search completed: February 4, 2004, 19:45:55
Job time : 151.409 secs
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 15:19:23 / Search time 1185.23 Seconds
(without alignments)
430.630 Million cell updates/sec

Title: US-09-744-875A-1

Sequence: 1 agattctcgaatcaatc 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 452990

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST.*
1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estuy:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_plh:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_prg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	16.2	77.1	82	9	Al218421	qh24b10.x		
2	15.2	72.4	57	14	CA333945	NISC_ly09		
3	15.2	72.4	84	28	AZ782789	2M0023P07		
4	15.2	72.4	87	14	CB405258	OSTR040A2		

C	5	15.2	72.4	91	29	Al940051	Arabidops
C	6	15.2	72.4	93	13	B0837156	B0837156
C	7	15.2	72.4	97	13	B0890262	P
C	8	14.6	69.5	73	9	AA749115	
C	9	14.6	69.5	93	29	B2593365	
C	10	14.4	68.6	63	9	AM695026	
C	11	14.4	68.6	93	14	CA513671	
C	12	14.4	68.6	97	28	A2437380	
C	13	14.2	67.6	48	28	BH851999	
C	14	14.2	67.6	60	10	BG153679	
C	15	14.2	67.6	83	9	AT966296	
C	16	13.8	65.7	47	12	B0771154	
C	17	13.8	65.7	49	9	AA422541	
C	18	13.8	65.7	69	28	A2810918	
C	19	13.8	65.7	69	28	A2956832	
C	20	13.8	65.7	76	10	BG153467	
C	21	13.8	65.7	82	10	BG151684	
C	22	13.8	65.7	88	10	BG151856	
C	23	13.8	65.7	88	29	BX533932	
C	24	13.8	65.7	91	14	CD028826	
C	25	13.8	65.7	91	28	AF087391	
C	26	13.8	65.7	91	28	BH758017	
C	27	13.6	64.8	48	28	BH615007	
C	28	13.6	64.8	50	10	BF789276	
C	29	13.6	64.8	63	10	BF463652	
C	30	13.6	64.8	71	10	BG668331	
C	31	13.6	64.8	81	13	B0890627	
C	32	13.6	64.8	86	9	AA863156	
C	33	13.6	64.8	87	29	BZ762984	
C	34	13.6	64.8	90	29	AL949242	
C	35	13.6	64.8	91	13	B0890255	
C	36	13.6	64.8	92	14	D75616	
C	37	13.6	64.8	94	28	BH218165	
C	38	13.6	64.8	96	12	BM181183	
C	39	13.6	64.8	96	29	CNS00JHH	
C	40	13.6	64.8	100	29	BZ352958	
C	41	13.4	63.8	44	29	BZ382706	
C	42	13.4	63.8	88	14	N73593	
C	43	13.4	63.8	100	9	AA420566	
C	44	13.2	62.9	49	29	BX178350	
C	45	13.2	62.9	52	9	AM697073	
C	46	13.2	62.9	61	28	BH218412	
C	47	13.2	62.9	72	13	B0754476	
C	48	13.2	62.9	76	9	AU011284	
C	49	13.2	62.9	78	28	AZ774680	
C	50	13.2	62.9	78	28	BH854811	
C	51	13.2	62.9	78	28	BH854812	
C	52	13.2	62.9	79	9	AT916764	
C	53	13.2	62.9	88	14	CD419293	
C	54	13.2	62.9	89	9	AW712808	
C	55	13.2	62.9	90	28	BH218396	
C	56	13.2	62.9	92	9	AU259036	
C	57	13.2	62.9	92	10	BE575638	
C	58	13.2	62.9	93	29	BZ663901	
C	59	13.2	62.9	93	9	AA877878	
C	60	13.2	62.9	94	9	AM518820	
C	61	13.2	62.9	95	29	AG265527	
C	62	13.2	62.9	96	28	BH251012	
C	63	13.2	62.9	97	12	BI942693	
C	64	13.2	62.9	100	28	BH170159	
C	65	13.2	62.9	100	28	BH867713	
C	66	13.2	62.9	41	29	BZ358843	
C	67	13.2	62.9	47	28	BH791798	
C	68	13.2	62.9	65	29	TA308040	
C	69	13.2	62.9	68	29	DR210925	
C	70	13.2	62.9	69	29	BZ593307	
C	71	13.2	62.9	74	28	AZ817173	
C	72	13.2	62.9	76	13	B0813172	
C	73	13.2	62.9	80	29	AL945129	
C	74	13.2	62.9	81	29	BZ593644	
C	75	13.2	62.9	83	28	BH609015	
C	76	13.2	62.9	84	29	BZ592972	
C	77	13.2	62.9	84	29	BZ706390	

78	13	61.9	85	29	BZ593630	BZ593630	SALK_0749	151	12.6	60.0	99	29	BZ383297	BZ383297	SALK_1324
79	13	61.9	86	29	BZ770275	BZ770275	SALK_1432	152	12.6	60.0	100	10	BE783348	BE783348	601471808
80	13	61.9	87	29	CC057344	CC057344	SALK_1403	153	12.6	60.0	100	14	CB981152	CB981152	CB70003
81	13	61.9	86	29	BX230484	BX230484	Danilo rer	154	12.6	60.0	100	14	BZ763312	BZ763312	SALK_1161
82	13	61.9	88	28	BH790508	BH790508	SALK_0572	155	12.4	59.0	27	14	L32053	L32053	HUMXP519A H
83	13	61.9	89	28	BZ593430	BZ593430	SALK_0704	156	12.4	59.0	39	12	BZ059042	BZ059042	BZ059042
84	13	61.9	90	29	BZ593470	BZ593470	SALK_0738	157	12.4	59.0	42	29	BZ664437	BZ664437	SALK_0712
85	13	61.9	91	28	BH813401	BH813401	SALK_0641	158	12.4	59.0	50	12	BM518218	BM518218	K189F07.Y
86	13	61.9	91	28	BZ592924	BZ592924	SALK_0513	159	12.4	59.0	54	28	BZ770934	BZ770934	SALK_1433
87	13	61.9	91	29	BZ593608	BZ593608	SALK_0749	160	12.4	59.0	56	28	AZ442536	AZ442536	IM0236R12
88	13	61.9	91	29	BZ593615	BZ593615	SALK_0749	161	12.4	59.0	58	28	AZ485203	AZ485203	IM0312D03
89	13	61.9	93	14	CA802671	CA802671	sauc40c07.	162	12.4	59.0	60	28	BH661876	BH661876	SALK_0882
90	13	61.9	93	29	BZ593225	BZ593225	SALK_0682	163	12.4	59.0	63	14	N66533	N66533	Y44G05..s1
91	13	61.9	93	29	BZ593350	BZ593350	SALK_0700	164	12.4	59.0	65	14	H91929	H91929	Y881C10..s1
92	13	61.9	94	10	BE317003	BE317003	NFO5BH03L	165	12.4	59.0	82	9	AL790753	AL790753	AL790753
93	13	61.9	94	29	BZ596785	BZ596785	SALK_0959	166	12.4	59.0	82	10	BE046924	BE046924	hd92e03.x
94	13	61.9	94	29	BZ597388	BZ597388	SALK_1035	167	12.4	59.0	88	13	BH817233	BH817233	UA14CPE04
95	13	61.9	94	29	BX203045	BX203045	Danilo rer	168	12.4	59.0	88	28	BH218207	BH218207	1006078A0
96	13	61.9	95	29	BZ593442	BZ593442	SALK_0738	169	12.4	59.0	96	10	BE316794	BE316794	NFO69C02L
97	13	61.9	95	29	BZ593481	BZ593481	SALK_0738	170	12.4	59.0	96	28	AL751939	AL751939	ArbIdops
98	13	61.9	96	9	AA129960	AA129960	zn86h07.r	171	12.2	58.1	36	28	B07685	B07685	CnC988 C-1
99	13	61.9	97	29	BZ592929	BZ592929	SALK_0513	172	12.2	58.1	38	12	BZ054304	BZ054304	BZ054304
100	13	61.9	97	29	BZ592939	BZ592939	SALK_0514	173	12.2	58.1	39	28	BH854070	BH854070	SALK_0786
101	13	61.9	97	29	BZ593339	BZ593339	SALK_0700	174	12.2	58.1	45	28	AZ815371	AZ815371	IM0503M04
102	13	61.9	98	29	BZ593393	BZ593393	SALK_0704	175	12.2	58.1	45	28	BH789555	BH789555	SALK_0378
103	13	61.9	98	29	BZ592970	BZ592970	SALK_0514	176	12.2	58.1	46	28	AZ807429	AZ807429	2M0070118
104	13	61.9	98	29	BZ596790	BZ596790	SALK_0960	177	12.2	58.1	50	9	AVB33464	AVB33464	AVB33464
105	13	61.9	99	29	BZ592969	BZ592969	SALK_0514	178	12.2	58.1	50	9	AW106260	AW106260	AW106260
106	13	61.9	100	9	AA790314	AA790314	vm81d12.r	179	12.2	58.1	55	28	AZ755909	AZ755909	ev10h02.x
107	13	61.9	100	9	AA123114	AA123114	mm30g03..r	180	12.2	58.1	55	28	AL760074	AL760074	ArbIdops
108	13	61.9	100	29	BZ593475	BZ593475	SALK_0738	181	12.2	58.1	55	29	BH609970	BH609970	HIV2SH07
109	13	61.9	100	29	BZ593514	BZ593514	SALK_0739	182	12.2	58.1	56	28	BH609970	BH609970	SALK_0390
110	12.8	61.0	55	14	CB279757	CB279757	ru86G06.Y	183	12.2	58.1	57	28	BH907277	BH907277	YK66G05..s
111	12.8	61.0	55	14	D19098	D19098	MUSG801305	184	12.2	58.1	58	9	AA546742	AA546742	YK66G05..s
112	12.8	61.0	79	10	BG151675	BG151675	na963B02.	185	12.2	58.1	60	29	AG217890	AG217890	na963B02.
113	12.8	61.0	79	12	BI749369	BI749369	ro77c09.Y	186	12.2	58.1	61	10	BC099703	BC099703	na963B02.
114	12.8	61.0	83	28	BH664231	BH664231	SALK_0956	187	12.2	58.1	62	10	BC099651	BC099651	na963B02.
115	12.8	61.0	83	29	BX285187	BX285187	ArbIdops	188	12.2	58.1	62	28	AZ779110	AZ779110	2M0015101
116	12.8	61.0	85	14	W68320	W68320	z35g12.r1	189	12.2	58.1	62	28	BH911348	BH911348	2M0015101
117	12.8	61.0	88	9	AA258670	AA258670	zr62g11..s	190	12.2	58.1	62	29	CC248960	CC248960	CC248960
118	12.8	61.0	97	28	BH213853	BH213853	SALK_0098	191	12.2	58.1	63	29	BE636462	BE636462	CC248960
119	12.8	61.0	99	10	AM891680	AM891680	CM3-NT009	192	12.2	58.1	64	10	BE199410	BE199410	CC248960
120	12.6	60.0	59	12	AG218403	AG218403	DJ058484	193	12.2	58.1	64	10	BH795569	BH795569	CC248960
121	12.6	60.0	59	12	BZ058484	BZ058484	SALK_0514	194	12.2	58.1	65	28	BH795569	BH795569	CC248960
122	12.6	60.0	59	28	BH232151	BH232151	1006166C1	195	12.2	58.1	68	28	AZ456722	AZ456722	CC248960
123	12.6	60.0	62	14	CB226387	CB226387	RT21G04.G	196	12.2	58.1	69	9	AW150050	AW150050	CC248960
124	12.6	60.0	63	14	BH866054	BH866054	SALK_1006	197	12.2	58.1	69	12	BZ065078	BZ065078	CC248960
125	12.6	60.0	63	28	BH230185	BH230185	1006156B0	198	12.2	58.1	69	29	BZ353323	BZ353323	CC248960
126	12.6	60.0	68	28	BH230185	BH230185	1006156B0	199	12.2	58.1	70	9	A1746314	A1746314	CC248960
127	12.6	60.0	72	13	BQ777631	BQ777631	113BH04.X	200	12.2	58.1	70	29	CC226111	CC226111	CC248960
128	12.6	60.0	79	9	AI958773	AI958773	fc96h07.Y	201	12.2	58.1	71	14	R52533	R52533	CC248960
129	12.6	60.0	80	9	AU277226	AU277226	fc96h07.Y	202	12.2	58.1	73	14	D18647	D18647	CC248960
130	12.6	60.0	81	28	AZ642707	AZ642707	IM0505B23	203	12.2	58.1	73	28	BH908930	BH908930	CC248960
131	12.6	60.0	81	28	BH625011	BH625011	1007102A0	204	12.2	58.1	74	29	AI223379	AI223379	CC248960
132	12.6	60.0	87	28	AZ598182	AZ598182	IM0412A21	205	12.2	58.1	74	29	AG248976	AG248976	CC248960
133	12.6	60.0	88	9	AA743211	AA743211	ny21b01.s	206	12.2	58.1	77	9	AI566444	AI566444	CC248960
134	12.6	60.0	90	13	BUT78554	BUT78554	1047A11.X	207	12.2	58.1	77	14	D19525	D19525	CC248960
135	12.6	60.0	90	14	CA948679	CA948679	1430C05.X	208	12.2	58.1	78	9	AA639781	AA639781	CC248960
136	12.6	60.0	90	14	CA950241	CA950241	1189602.X	209	12.2	58.1	78	14	CB818341	CB818341	CC248960
137	12.6	60.0	90	14	AZ629593	AZ629593	IM0482L09	210	12.2	58.1	78	14	BX140455	BX140455	CC248960
138	12.6	60.0	91	14	CB069621	CB069621	1525H05.X	211	12.2	58.1	78	29	AI854995	AI854995	CC248960
139	12.6	60.0	91	14	D19910	D19910	HUMGS00867	212	12.2	58.1	81	9	AL854995	AL854995	CC248960
140	12.6	60.0	91	14	W05611	W05611	za85f05..r1	213	12.2	58.1	82	9	AL624782	AL624782	CC248960
141	12.6	60.0	92	14	CA935578	CA935578	sa856C04.	214	12.2	58.1	82	12	BM341911	BM341911	CC248960
142	12.6	60.0	93	28	AL769421	AL769421	AY127421	215	12.2	58.1	82	28	AZ612702	AZ612702	CC248960
143	12.6	60.0	93	28	AL769421	AL769421	AY127421	216	12.2	58.1	82	28	BH415412	BH415412	CC248960
144	12.6	60.0	95	28	BH230248	BH230248	1006156H0	217	12.2	58.1	83	28	AZ483795	AZ483795	CC248960
145	12.6	60.0	95	29	BZ593231	BZ593231	SALK_0682	218	12.2	58.1	83	28	BH755898	BH755898	CC248960
146	12.6	60.0	96	28	BX003033	BX003033	ArbIdops	219	12.2	58.1	84	10	BG151589	BG151589	CC248960
147	12.6	60.0	96	28	AZ917909	AZ917909	1006002E0	220	12.2	58.1	85	29	BZ770934	BZ770934	CC248960
148	12.6	60.0	96	28	BH230199	BH230199	1006156F0	221	12.2	58.1	86	29	BX246757	BX246757	CC248960
149	12.6	60.0	96	28	BH909364	BH909364	SALK_0531	222	12.2	58.1	87	9	AA692589	AA692589	CC248960
150	12.6	60.0	96	28	BH909364	BH909364	SALK_0531	223	12.2	58.1	87	9	AA692589	AA692589	CC248960

BZ383297	SALK_1324	BE783348	601471808	CB981152	CB70003	BZ763312	SALK_1161	I12053	HUMXP519A H	BZ059042	BZ059042	BZ664437	SALK_0712	BM518218	K189F07.Y	BZ770934	SALK_1433	AZ442536	IM0236R12	AZ485203	IM0312D03	BH661876	SALK_0882	N66533	Y44G05..s1	H91929	Y881C10..s1	AL790753	AL790753	BE046924	hd92e03.x	BH817233	UA14CPE04	BH218207	1006078A0	BH16794	NFO69C02L	AL751939	ArbIdops	B07685	CnC988 C-1	BZ054304	BZ054304	BH854070	SALK_0786	AZ815371	IM0503M04	BH789555	SALK_0378	AZ807429	2M0070118	AVB33464	AVB33464	AW106260	AW106260	AZ755909	ev10h02.x	AL760074	ArbIdops	BH609970	HIV2SH07	BH907277	SALK_0390	YK66G05..s	YK66G05..s	AG217890	DJ058484	BC099703	na963B02.	BC099651	na963B02.	AZ779110	2M0015101	BH911348	SALK_0677	CC248960	CC177 Bay	BE636462	SMOV3MCM	BE199410	SMOV3MCM	BZ755659	10
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224	12.2	58.1	87	14	CA047445	CA047445 ssalpic15	297	12	57.1	68	28	BH080781	BH080781 100808201
225	12.2	58.1	88	9	AI457452	AI457452 cl73f04.x	298	12	57.1	70	9	AW105596	AW105596 xdx3408.x
226	12.2	58.1	88	12	BI322201	BI322201 kx17g05.y	299	12	57.1	70	12	BI700718	BI700718 sa128c04.
227	12.2	58.1	88	28	AZ416906	AZ416906 lM0192B21	300	12	57.1	70	29	AL948250	AL948250 Arbibdops
228	12.2	58.1	88	29	DR3124S	AL740179 Danilo rer	301	12	57.1	71	9	AA852647	AA852647 NHTBca15
229	12.2	58.1	90	10	BE023791	BE023791 sm92e01.y	302	12	57.1	72	9	AU011466	AU011466 AU011466
230	12.2	58.1	90	29	BZ596774	BZ596774 SALK 0959	303	12	57.1	72	14	CB358158	CB358158 ZF001-P00
231	12.2	58.1	90	29	BX227157	BX227157 Danilo rer	304	12	57.1	73	14	CB833331	CB833331 SWBmfcAV
232	12.2	58.1	91	9	AA886069	AA886069 ny40e08.s	305	12	57.1	73	14	CD400293	CD400293 gm ck2213
233	12.2	58.1	91	10	BG151628	BG151628 na6e2d01.	306	12	57.1	74	9	AA961856	AA961856 orgf01.s
234	12.2	58.1	92	14	H38218	H38218 yp58c08.s1	307	12	57.1	74	14	N91232	N91232 zai3h05.f1
235	12.2	58.1	92	14	H33998	R33998 yf73g03.s1	308	12	57.1	74	28	BH609000	BH609000 19h20.L11
236	12.2	58.1	93	9	AI759845	AI759845 sb65f12.y	309	12	57.1	75	9	AT291829	AT291829 qm80g09.x
237	12.2	58.1	93	9	AA220296	AA220296 mv69f12.y	310	12	57.1	75	9	AA235745	AA235745 zsa40a2.r
238	12.2	58.1	93	12	BM642821	BM642821 fwa4d05.y	311	12	57.1	75	13	BQ454048	BQ454048 sa075a11.
239	12.2	58.1	93	12	BM342821	BM342821 SALK 0265	312	12	57.1	75	28	AF020742	AF020742 AF020742
240	12.2	58.1	93	29	BZ665053	AF211647 AF211647	313	12	57.1	75	14	D19177	D19177 MOSGS00445
241	12.2	58.1	94	9	AA261910	AA261910 zsl7d07.s	314	12	57.1	76	14	D19177	D19177 MOSGS00445
242	12.2	58.1	94	9	AV534948	AV534948 AV534948	315	12	57.1	77	28	AZ833051	AZ833051 2M0113B23
243	12.2	58.1	94	28	BH609051	BH609051 21f1.L118	316	12	57.1	78	28	BH790531	BH790531 SALK 0572
244	12.2	58.1	95	9	AT759885	AT759885 sb65f06.y	317	12	57.1	79	28	AZ346857	AZ346857 1M0082016
245	12.2	58.1	95	29	AL766559	AL766559 Arbibdops	318	12	57.1	80	9	AL876324	AL876324 AL876324
246	12.2	58.1	95	29	AF211554	AF211554 AF211554	319	12	57.1	81	29	AL951911	AL951911 Arbibdops
247	12.2	58.1	96	9	AV970576	AV970576 AV970576	320	12	57.1	81	29	AL951911	AL951911 Arbibdops
248	12.2	58.1	96	12	BM067985	BM067985 KS08015B0	321	12	57.1	82	9	AM546050	AM546050 l0001F05-
249	12.2	58.1	97	12	BG151971	BG151971 na66g011.	322	12	57.1	82	14	CB221341	CB221341 lDu002G12
250	12.2	58.1	98	29	BX205037	BX205037 Danilo rer	323	12	57.1	83	9	AL193269	AL193269 ge57a03.x
251	12.2	58.1	98	29	BX205037	BX205037 Danilo rer	324	12	57.1	83	9	AV518809	AV518809 AV518809
252	12.2	58.1	100	12	BI011456	BI011456 QV2-ENM09	325	12	57.1	84	9	AA823746	AA823746 v61809.s
253	12.2	58.1	100	12	BI011457	BI011457 QV2-ENM09	326	12	57.1	84	28	BG406002	BG406002 sac40g10.
254	12.2	58.1	100	12	BI011457	BI011457 QV2-ENM09	327	12	57.1	84	28	AZ462719	AZ462719 1M0271108
255	12.2	58.1	100	12	BI011691	BI011691 QV2-ENM09	328	12	57.1	84	28	AZ806807	AZ806807 2M0069C07
256	12.2	58.1	100	12	BI011692	BI011692 QV2-ENM09	329	12	57.1	84	29	BZ762189	BZ762189 SALK 0920
257	12.2	58.1	100	12	BI011748	BI011748 QV2-ENM09	330	12	57.1	85	29	BE316364	BE316364 NF0330011
258	12.2	58.1	100	12	BI011749	BI011749 QV2-ENM09	331	12	57.1	85	29	AL753726	AL753726 Arbibdops
259	12.2	58.1	100	28	AZ659734	AZ659734 1M0537B21	332	12	57.1	86	9	AA674031	AA674031 vp70d1.r
260	12.2	57.1	29	28	AZ773589	AZ773589 2M0001B18	333	12	57.1	86	29	BZ289123	BZ289123 SALK 0225
261	12.2	57.1	30	28	BH861138	BH861138 SALK 0344	334	12	57.1	87	28	AZ595920	AZ595920 1M0408C23
262	12.2	57.1	30	28	BZ769653	BZ769653 SALK_1425	335	12	57.1	87	29	BZ661449	BZ661449 SALK 0249
263	12.2	57.1	39	29	AL943780	AL943780 Arbibdops	336	12	57.1	88	14	R86649	R86649 RABSTJ34T
264	12.2	57.1	40	29	AL755033	AL755033 Arbibdops	337	12	57.1	88	28	BH791490	BH791490 SALK 0600
265	12.2	57.1	41	29	BZ384956	BZ384956 SALK 1362	338	12	57.1	88	29	BZ593578	BZ593578 vv29C08.r
266	12.2	57.1	44	28	AZ603456	AZ603456 1M0422G09	339	12	57.1	89	9	AA667325	AA667325 v729C08.r
267	12.2	57.1	45	29	AL758755	AL758755 Arbibdops	340	12	57.1	89	9	AA667325	AA667325 v729C08.r
268	12.2	57.1	48	29	BX288143	BX288143 Arbibdops	341	12	57.1	89	12	BJ032888	BJ032888 AL778537
269	12.2	57.1	50	9	AU106259	AU106259 Arbibdops	342	12	57.1	90	9	AL778537	AL778537 AL778537
270	12.2	57.1	51	28	AZ787787	AZ787787 2M0034A01	343	12	57.1	90	9	AM516235	AM516235 xt63b10.x
271	12.2	57.1	52	28	AZ389475	AZ389475 1M0150I02	344	12	57.1	92	9	AM516235	AM516235 xt63b10.x
272	12.2	57.1	53	9	AU254941	AU254941 SALK 1260	345	12	57.1	92	14	T67128	T67128 ya52h12.s4
273	12.2	57.1	53	29	BZ354914	BZ354914 Arbibdops	346	12	57.1	93	28	AZ421821	AZ421821 1M0200D15
274	12.2	57.1	53	29	BX289503	BX289503 Arbibdops	347	12	57.1	93	28	AZ478111	AZ478111 1M0297022
275	12.2	57.1	54	28	AZ352619	AZ352619 1M0091111	348	12	57.1	94	9	AA904411	AA904411 ok07d11.s
276	12.2	57.1	54	29	CC458598	CC458598 SALK 1211	349	12	57.1	94	9	AA464530	AA464530 xk85a03.b
277	12.2	57.1	55	9	AA413252	AA413252 v652e05.r	350	12	57.1	94	10	BE978017	BE978017 DB72C09.y
278	12.2	57.1	55	9	AA413252	AA413252 v652e05.r	351	12	57.1	94	28	AZ628724	AZ628724 1M0481A09
279	12.2	57.1	57	29	AL941671	AL941671 Arbibdops	352	12	57.1	95	9	AM022202	AM022202 dE34C06.y
280	12.2	57.1	58	12	BM892848	BM892848 sam4a06.	353	12	57.1	95	28	AZ312826	AZ312826 1M0028120
281	12.2	57.1	59	9	AF090227	AF090227 Arbibdops	354	12	57.1	96	12	BM114147	BM114147 ACS96-JM3
282	12.2	57.1	60	9	AF090541	AF090541 zj92e06.s	355	12	57.1	96	28	AZ448143	AZ448143 1M0245108
283	12.2	57.1	62	28	BH904381	BH904381 SALK 1043	356	12	57.1	96	28	AZ485525	AZ485525 1M0390G14
284	12.2	57.1	63	29	BZ354428	BZ354428 SALK 1251	357	12	57.1	97	28	AZ427365	AZ427365 1M0209115
285	12.2	57.1	63	9	AM250422	AM250422 28226F4.3	358	12	57.1	97	29	AA683398	AA683398 SALK 1338
286	12.2	57.1	64	10	B02268	B02268 GSRL-150G1-	359	12	57.1	98	9	AA683398	AA683398 v706e02.r
287	12.2	57.1	64	10	B02268	B02268 GSRL-150G1-	360	12	57.1	98	14	CB219237	CB219237 vaa09h10.
288	12.2	57.1	65	28	BE154383	BE154383 SMOV3CAN	361	12	57.1	99	9	AI928311	AI928311 w012d05.x
289	12.2	57.1	65	28	AZ464196	AZ464196 1M0273024	362	12	57.1	99	10	BG099714	BG099714 na9569Y01.
290	12.2	57.1	66	14	CB298764	CB298764 220022.re	363	12	57.1	99	28	AZ663311	AZ663311 1M0542F20
291	12.2	57.1	66	28	AZ653097	AZ653097 1M0526B12	364	12	57.1	100	9	AT006416	AT006416 AT006416
292	12.2	57.1	67	28	B46127	B46127 HS-1063-A1-	365	12	57.1	100	9	AA222761	AA222761 mw99f10.r
293	12.2	57.1	67	28	AZ693625	AZ693625 AST-2HB3	366	12	57.1	100	10	BG059770	BG059770 naF53e02.
294	12.2	57.1	67	28	BH904507	BH904507 SALK 1043	367	12	57.1	100	10	BE168257	BE168257 QV3-HT051
295	12.2	57.1	67	29	BX290793	BX290793 Arbibdops	368	12	57.1	100	10	BE168257	BE168257 QV3-HT051
296	12.2	57.1	67	29	AL483629	AL483629 T. Brucei	369	12	57.1	100	10	BE168257	BE168257 QV3-HT051
297	12.2	57.1	68	9	AM089371	AM089371 xdx03h01.x	369	12	57.1	100	10	BE168257	BE168257 QV3-HT051

Thu Feb

370	12	57.1	100	14	CD016928	443	11.6	55.2	49	9	AV856952
371	12	57.1	100	14	L47086	444	11.6	55.2	50	29	BZ290769
372	12	57.1	100	28	AZ499868	445	11.6	55.2	50	29	BZ766694
373	12	57.1	100	28	AZ871636	446	11.6	55.2	51	14	CD287068
374	12	57.1	100	29	BX285144	447	11.6	55.2	52	9	AA671557
375	11.8	56.2	49	29	BX341744	448	11.6	55.2	52	14	D19970
376	11.8	56.2	49	29	BZ382279	449	11.6	55.2	54	29	CC054889
377	11.8	56.2	51	9	AI874330	450	11.6	55.2	55	28	BH909014
378	11.8	56.2	51	28	BH861217	451	11.6	55.2	56	28	BH910542
379	11.8	56.2	55	9	AV679652	452	11.6	55.2	56	29	AL761721
380	11.8	56.2	57	12	BJ060934	453	11.6	55.2	57	29	BX288722
381	11.8	56.2	61	9	AA797809	454	11.6	55.2	58	13	BUT63912
382	11.8	56.2	61	28	BH813589	455	11.6	55.2	58	28	AZ834761
383	11.8	56.2	69	28	BH866285	456	11.6	55.2	58	28	BH757984
384	11.8	56.2	70	28	AZ767286	457	11.6	55.2	58	29	CC456103
385	11.8	56.2	70	29	BZ662724	458	11.6	55.2	58	29	BX003656
386	11.8	56.2	72	29	AL766711	459	11.6	55.2	60	9	AI001444
387	11.8	56.2	73	10	AM600127	460	11.6	55.2	60	9	AI024866
388	11.8	56.2	73	10	BF400551	461	11.6	55.2	60	10	BF638938
389	11.8	56.2	74	29	BF228803	462	11.6	55.2	60	10	BE317722
390	11.8	56.2	74	29	CC019286	463	11.6	55.2	61	9	AU264739
391	11.8	56.2	78	9	AI538324	464	11.6	55.2	61	29	BX132821
392	11.8	56.2	78	9	AM444383	465	11.6	55.2	62	28	B02404
393	11.8	56.2	79	12	BG922421	466	11.6	55.2	62	28	BH865963
394	11.8	56.2	82	9	AA937053	467	11.6	55.2	63	12	BH092661
395	11.8	56.2	82	28	AA311258	468	11.6	55.2	63	12	AL764604
396	11.8	56.2	83	28	AZ313453	469	11.6	55.2	64	10	FL184766
397	11.8	56.2	84	29	BZ770383	470	11.6	55.2	64	12	BI142453
398	11.8	56.2	85	12	BH955577	471	11.6	55.2	64	28	AZ767737
399	11.8	56.2	85	29	BZ382918	472	11.6	55.2	65	9	AA663663
400	11.8	56.2	86	9	AI624578	473	11.6	55.2	65	29	BZ768337
401	11.8	56.2	86	29	BZ287287	474	11.6	55.2	66	28	BH856058
402	11.8	56.2	86	29	CC459452	475	11.6	55.2	67	28	BH909567
403	11.8	56.2	87	9	AA606997	476	11.6	55.2	68	29	AL762542
404	11.8	56.2	87	29	AL761605	477	11.6	55.2	69	9	AI1318263
405	11.8	56.2	88	9	AA879169	478	11.6	55.2	69	9	AM101936
406	11.8	56.2	88	12	BJ040608	479	11.6	55.2	69	28	BH229731
407	11.8	56.2	90	10	BH026989	480	11.6	55.2	69	28	BH811031
408	11.8	56.2	90	14	H62362	481	11.6	55.2	70	9	AV531112
409	11.8	56.2	90	28	BH086922	482	11.6	55.2	70	14	CB305238
410	11.8	56.2	90	28	BZ352622	483	11.6	55.2	71	13	B0548401
411	11.8	56.2	90	29	CNS00NT9	484	11.6	55.2	71	13	B0627408
412	11.8	56.2	90	29	DME545165	485	11.6	55.2	71	28	BH640591
413	11.8	56.2	94	12	BM155838	486	11.6	55.2	71	28	BH662544
414	11.8	56.2	96	28	AF166318	487	11.6	55.2	71	29	CC057459
415	11.8	56.2	96	28	AZ345753	488	11.6	55.2	71	29	AL950435
416	11.8	56.2	97	28	BH902662	489	11.6	55.2	72	9	AA804887
417	11.8	56.2	98	28	AZ781382	490	11.6	55.2	73	9	AI970998
418	11.8	56.2	99	10	BH589742	491	11.6	55.2	73	10	BG485870
419	11.8	56.2	100	14	AU012857	492	11.6	55.2	73	10	BF172293
420	11.8	56.2	100	28	BH619409	493	11.6	55.2	73	12	BI107307
421	11.8	56.2	100	28	BH619409	494	11.6	55.2	73	12	BI499209
422	11.6	55.2	33	29	BZ593776	495	11.6	55.2	74	10	BG326571
423	11.6	55.2	34	9	AI222055	496	11.6	55.2	74	12	BI697935
424	11.6	55.2	35	12	BJ034960	497	11.6	55.2	74	12	BI697935
425	11.6	55.2	35	28	BH911632	498	11.6	55.2	74	13	BI788738
426	11.6	55.2	37	9	AI695230	499	11.6	55.2	75	2	B0824712
427	11.6	55.2	37	9	AI791737	500	11.6	55.2	75	9	AA656643
428	11.6	55.2	37	9	AL778643	501	11.6	55.2	75	9	AI544695
429	11.6	55.2	37	9	AL778681	502	11.6	55.2	75	9	AA251076
430	11.6	55.2	37	9	AL780719	503	11.6	55.2	75	9	AA618851
431	11.6	55.2	37	9	AL781888	504	11.6	55.2	75	28	AF524263
432	11.6	55.2	40	9	AI019078	505	11.6	55.2	76	9	AI1365309
433	11.6	55.2	40	28	BH865961	506	11.6	55.2	78	28	BH791742
434	11.6	55.2	40	28	BH865962	507	11.6	55.2	79	9	AM088441
435	11.6	55.2	40	28	BH865962	508	11.6	55.2	79	13	BQ268662
436	11.6	55.2	41	29	BZ384839	509	11.6	55.2	79	13	BQ268662
437	11.6	55.2	41	29	AL943061	510	11.6	55.2	79	28	AZ763244
438	11.6	55.2	43	29	AL768905	511	11.6	55.2	79	29	AL761679
439	11.6	55.2	44	29	BZ290725	512	11.6	55.2	80	9	AA887426
440	11.6	55.2	44	28	BH847193	513	11.6	55.2	80	9	AF054915
441	11.6	55.2	48	29	BZ379558	514	11.6	55.2	80	9	AI211610
442	11.6	55.2	48	29	BX003722	515	11.6	55.2	80	9	AU007559

C 516	11.6	55.2	80 13	B0875615	B0875615 V009C02 P	C 589	11.6	55.2	99 12	B0997532
C 517	11.6	55.2	81 9	AL850542	AL850542	C 590	11.6	55.2	99 28	A2435835
C 518	11.6	55.2	81 10	BG515353	BG515353 dae04c01.	C 591	11.6	55.2	99 28	A2456475
C 519	11.6	55.2	81 12	BH436075	BH436075 IRK20E1.a	C 592	11.6	55.2	99 28	BH910534
C 520	11.6	55.2	81 14	CA856618	CA856618 PESTOac1	C 593	11.6	55.2	99 29	CC455417
C 521	11.6	55.2	82 9	AJ499243	AJ499243 AJ499243	C 594	11.6	55.2	99 29	CC455126
C 522	11.6	55.2	82 28	BH909257	BH909257 SALK_0526	C 595	11.6	55.2	99 29	AG242456
C 523	11.6	55.2	82 29	CC056562	CC056562 SALK_1087	C 596	11.6	55.2	100 9	AA474231
C 524	11.6	55.2	82 29	CC456294	CC456294 SALK_0970	C 597	11.6	55.2	100 10	BG142713
C 526	11.6	55.2	83 9	AA606588	AA606588 vm8b03.r	C 598	11.6	55.2	100 10	BG657485
C 528	11.6	55.2	83 29	CC179387	CC179387 SALK_0681	C 599	11.6	55.2	100 10	BE074143
C 529	11.6	55.2	84 9	AL942410	AL942410 Arabidops	C 600	11.6	55.2	100 14	CA844442
C 530	11.6	55.2	84 12	BM276486	BM276486 PESTOac8	C 601	11.6	55.2	100 14	CA844430
C 531	11.6	55.2	84 13	B0866619	B0866619 S068H03 P	C 602	11.4	54.3	23 29	BZ357850
C 532	11.6	55.2	84 14	CA854531	CA854531 PESTOac3	C 603	11.4	54.3	26 28	BH903468
C 533	11.6	55.2	84 28	BH910242	BH910242 SALK_0585	C 604	11.4	54.3	32 28	AZ793545
C 534	11.6	55.2	85 14	AA968880	AA968880 op37hi2.s	C 605	11.4	54.3	33 28	AZ340354
C 535	11.6	55.2	85 14	CD415624	CD415624 GM_CK5805	C 606	11.4	54.3	34 28	BH813789
C 537	11.6	55.2	85 28	BH908345	BH908345 SALK_0474	C 607	11.4	54.3	35 28	AZ345589
C 538	11.6	55.2	86 9	A1462833	A1462833 vb37d01.x	C 608	11.4	54.3	36 29	TA113E05Q
C 539	11.6	55.2	86 9	A1538919	A1538919 cp75a02.x	C 610	11.4	54.3	37 9	AU254721
C 540	11.6	55.2	86 9	A1538919	A1538919 cp75a02.x	C 611	11.4	54.3	39 28	BH907039
C 541	11.6	55.2	86 28	BH906369	BH906369 SALK_1097	C 612	11.4	54.3	44 28	BH789203
C 542	11.6	55.2	86 28	BH906370	BH906370 SALK_1097	C 613	11.4	54.3	44 28	AL952779
C 543	11.6	55.2	86 28	BH906371	BH906371 SALK_1097	C 614	11.4	54.3	46 28	AZ777964
C 544	11.6	55.2	86 29	DM546313	DM546313 Drosophila	C 615	11.4	54.3	48 29	BZ595374
C 545	11.6	55.2	87 9	A1597718	A1597718 tui5h01.x	C 616	11.4	54.3	49 9	AU007710
C 546	11.6	55.2	87 9	AV534789	AV534789 AV534789	C 617	11.4	54.3	50 9	BM636470
C 547	11.6	55.2	87 12	BM053015	BM053015 i669c01.y	C 618	11.4	54.3	50 9	AU101093
C 548	11.6	55.2	87 28	BH851607	BH851607 SALK_0732	C 619	11.4	54.3	50 28	AU103386
C 549	11.6	55.2	87 29	BZ660879	BZ660879 SALK_0243	C 620	11.4	54.3	50 28	BH866406
C 550	11.6	55.2	88 29	BZ767672	BZ767672 EST235124	C 621	11.4	54.3	51 29	AL753784
C 551	11.6	55.2	88 29	A1406837	A1406837 SALK_1391	C 622	11.4	54.3	52 29	BZ292315
C 552	11.6	55.2	89 9	A1523226	A1523226 ar70d07.x	C 623	11.4	54.3	52 29	BZ292316
C 553	11.6	55.2	89 9	AA442834	AA442834 g3f1me7.x	C 624	11.4	54.3	54 9	AA654697
C 554	11.6	55.2	89 14	CB885113	CB885113 Ma230404	C 625	11.4	54.3	55 9	AL440743
C 555	11.6	55.2	89 29	BZ767670	BZ767670 SALK_1391	C 626	11.4	54.3	55 9	AA659546
C 556	11.6	55.2	90 9	A1656705	A1656705 t47d12.x	C 627	11.4	54.3	57 28	BH636414
C 558	11.6	55.2	90 9	AM080543	AM080543 xc24d11.x	C 628	11.4	54.3	57 29	AL945826
C 559	11.6	55.2	90 9	AM693694	AM693694 NP668R03S	C 629	11.4	54.3	58 9	AA908441
C 560	11.6	55.2	91 9	A1020565	A1020565 ua96a08.r	C 630	11.4	54.3	59 9	A1451268
C 561	11.6	55.2	91 9	A1086512	A1086512 oz60c08.x	C 631	11.4	54.3	60 29	BZ380224
C 562	11.6	55.2	91 9	AU071129	AU071129 AU071129	C 632	11.4	54.3	61 9	AA460636
C 563	11.6	55.2	91 10	BF695130	BF695130 su75d11.Y	C 633	11.4	54.3	61 14	D18665
C 564	11.6	55.2	91 10	BF604369	BF604369 SMOVAFCAD	C 634	11.4	54.3	62 9	AM073526
C 565	11.6	55.2	91 14	D18617	D18617 MUSGS01678	C 635	11.4	54.3	62 10	BG099651
C 566	11.6	55.2	92 9	A1110529	A1110529 SMOVL3CAN	C 636	11.4	54.3	63 29	AG265691
C 567	11.6	55.2	92 14	CB165114	CB165114 44 Alifalt	C 637	11.4	54.3	64 10	AM749322
C 568	11.6	55.2	92 28	BH856181	BH856181 SALK_0832	C 638	11.4	54.3	64 12	B1097367
C 569	11.6	55.2	93 9	AA884587	AA884587 am38d07.s	C 639	11.4	54.3	64 14	C02331
C 570	11.6	55.2	94 9	AA720433	AA720433 SMOVL3CAN	C 640	11.4	54.3	65 14	T56691
C 571	11.6	55.2	94 29	BZ666241	BZ666241 SGT5083-3	C 641	11.4	54.3	65 28	BH418348
C 572	11.6	55.2	95 9	AU258044	AU258044 AU258044	C 642	11.4	54.3	68 28	BH789943
C 573	11.6	55.2	95 13	BUD06520	BUD06520 604151889	C 643	11.4	54.3	68 28	BZ662588
C 574	11.6	55.2	95 14	H61099	H61099 yf51c12.r1	C 644	11.4	54.3	68 29	BH789943
C 575	11.6	55.2	95 28	BH864029	BH864029 SALK_0951	C 645	11.4	54.3	69 28	AZ810513
C 576	11.6	55.2	96 28	BH223697	BH223697 1006114D1	C 646	11.4	54.3	69 29	BZ584508
C 577	11.6	55.2	97 9	AL709297	AL709297 at02a08.x	C 647	11.4	54.3	70 13	B0592241
C 578	11.6	55.2	97 9	AL783986	AL783986 AL783986	C 648	11.4	54.3	71 28	AL757525
C 579	11.6	55.2	98 9	AV963943	AV963943 AV963943	C 649	11.4	54.3	72 28	BH846622
C 580	11.6	55.2	98 10	BF632171	BF632171 NF018G06D	C 650	11.4	54.3	72 29	BX290034
C 581	11.6	55.2	98 10	BE042421	BE042421 ho18g01.x	C 651	11.4	54.3	73 10	AM874908
C 582	11.6	55.2	98 12	BM984192	BM984192 UT-CF-D01	C 652	11.4	54.3	73 28	AA050026
C 583	11.6	55.2	98 14	CA844389	CA844389 JPSSRG_2A	C 653	11.4	54.3	73 29	AL944498
C 584	11.6	55.2	98 14	CA844390	CA844390 JPSSRG_2B	C 654	11.4	54.3	74 9	AL448781
C 585	11.6	55.2	98 14	CA844390	CA844390 JPSSRG_2B	C 655	11.4	54.3	74 12	B0066433
C 586	11.6	55.2	98 28	BH632443	BH632443 1007095D0	C 656	11.4	54.3	74 29	BZ290450
C 587	11.6	55.2	98 28	BH789947	BH789947 SALK_0528	C 657	11.4	54.3	74 29	BX288293
C 588	11.6	55.2	98 29	BZ533365	BZ533365 SALK_1202	C 658	11.4	54.3	75 9	AM597097
C 589	11.6	55.2	99 10	BF146464	BF146464 uy29c09.x	C 659	11.4	54.3	75 9	AA915292
C 590	11.6	55.2	99 12	BG997532	BG997532 PM0-HT091	C 660	11.4	54.3	76 9	AM059619
C 591	11.6	55.2	99 28	AZ435835	AZ435835 IM0223C08	C 661	11.4	54.3	76 9	AM059619
C 592	11.6	55.2	99 28	AZ456475	AZ456475 IM0259C08					
C 593	11.6	55.2	99 28	BH910534	BH910534 SALK_0601					
C 594	11.6	55.2	99 29	CC455417	CC455417 SALK_0821					
C 595	11.6	55.2	99 29	CC455126	CC455126 SALK_0936					
C 596	11.6	55.2	100 9	AA474231	AA474231 veg1c07.r					
C 597	11.6	55.2	100 10	BG142713	BG142713 TgBETzya2					
C 598	11.6	55.2	100 10	BG657485	BG657485 TgBETzya2					
C 599	11.6	55.2	100 14	CA844442	CA844442 BSSSRG_1B					
C 600	11.6	55.2	100 14	CA844430	CA844430 BSSSRG_1C					
C 601	11.6	55.2	100 14	CA844430	CA844430 BSSSRG_1C					
C 602	11.4	54.3	23 29	BZ357850	BZ357850 SALK_1313					
C 603	11.4	54.3	26 28	BH903468	BH903468 SALK_1026					
C 604	11.4	54.3	32 28	AZ793545	AZ793545 2M0012C23					
C 605	11.4	54.3	33 28	AZ340354	AZ340354 1M0072P06					
C 606	11.4	54.3	34 28	BH813789	BH813789 SALK_0653					
C 607	11.4	54.3	35 28	AZ345589	AZ345589 1M0080N16					
C 608	11.4	54.3	36 29	TA113E05Q	TA113E05Q T. brucei					
C 609	11.4	54.3	37 9	AU254721	AU254721 AU254721					
C 610	11.4	54.3	39 28	BH907039	BH907039 SALK_0375					
C 611	11.4	54.3	44 28	BH789203	BH789203 SALK_0009					
C 612	11.4	54.3	44 28	AL952779	AL952779 Arabidops					
C 613	11.4	54.3	46 28	AZ777964	AZ777964 2M0012C23					
C 614	11.4	54.3	48 29	BZ595374	BZ595374 SALK_0869					
C 615	11.4	54.3	49 9	AU007710	AU007710 AU007710					
C 616	11.4	54.3	50 9	BM636470	BM636470 1008011E0					
C 617	11.4	54.3	50 9	AU101093	AU101093 AU101093					
C 618	11.4	54.3	50 28	AU103386	AU103386 AU103386					
C 619	11.4	54.3	50 28	BH866406	BH866406 SALK_1012					
C 620	11.4	54.3	51 29	AL753784	AL753784 Arabidops					
C 621	11.4	54.3	52 29	BZ292315	BZ292315 SALK_1237					
C 622	11.4	54.3	52 29	BZ292316	BZ292316 SALK_1238					
C 623	11.4	54.3	54 9	AA654697	AA654697 nt73d03.s					
C 624	11.4	54.3	55 9	AL440743	AL440743 sb53d06.y					
C 625	11.4	54.3	55 9	AA659546	AA659546 vf67d07.r					
C 626	11.4	54.3	57 28	BH636414	BH636414 1008011B1					
C 627	11.4	54.3	57 29	AL945826	AL945826 Arabidops					
C 628	11.4	54.3	58 9	AA908441	AA908441 og78f10.s					
C 629	11.4	54.3	59 9	A1451268	A1451268 mt75c01.x					
C 630	11.4	54.3	60 29	BZ380224	BZ380224 SALK_1148					

662	11.4	54.3	76	28	BH866100	SALK_1007	C 735	11.4	54.3	97	29	EX003083
663	11.4	54.3	76	29	AL942915	ArabiDops	C 736	11.4	54.3	98	9	AW466364
664	11.4	54.3	77	28	BH907838	SALK_0443	C 737	11.4	54.3	98	9	AA536938
665	11.4	54.3	77	29	AL771723	ArabiDops	C 738	11.4	54.3	98	10	BG513161
666	11.4	54.3	78	9	AI930938	AL930938 sb44h1.y	C 739	11.4	54.3	98	14	TE60914
667	11.4	54.3	78	14	CD407904	Gm_CK3366	C 740	11.4	54.3	98	28	AF149441
668	11.4	54.3	78	29	CC055730	CC055730 SALK_0473	C 741	11.4	54.3	98	28	AZ308835
669	11.4	54.3	79	28	BG085632	BG085632 H3115F07	C 742	11.4	54.3	98	28	BH813207
670	11.4	54.3	79	28	AZ584347	AZ584347 IM0388014	C 743	11.4	54.3	98	29	CC035140
671	11.4	54.3	79	29	CNS07FEL	AL608619 Anophelies	C 744	11.4	54.3	99	28	BH905685
672	11.4	54.3	80	9	AMS48563	AMS48563 L0038E09	C 745	11.4	54.3	99	28	CC035140
673	11.4	54.3	80	28	AMS48563	AMS48563 L0038E09	C 746	11.4	54.3	99	28	BH905685
674	11.4	54.3	81	9	AMS48563	AMS48563 L0038E09	C 747	11.4	54.3	99	28	BH905685
675	11.4	54.3	81	28	AMS48563	AMS48563 L0038E09	C 748	11.4	54.3	99	28	BH905685
676	11.4	54.3	81	29	AMS48563	AMS48563 L0038E09	C 749	11.4	54.3	99	28	BH905685
677	11.4	54.3	82	9	AMS48563	AMS48563 L0038E09	C 750	11.4	54.3	100	9	AA063930
678	11.4	54.3	82	9	AMS48563	AMS48563 L0038E09	C 751	11.4	54.3	100	9	AA063930
679	11.4	54.3	82	9	AMS48563	AMS48563 L0038E09	C 752	11.4	54.3	100	9	AA063930
680	11.4	54.3	82	28	BH230418	BH230418 L006157H0	C 753	11.4	54.3	100	10	BE057596
681	11.4	54.3	82	29	AL943645	AL943645 ArabiDops	C 754	11.4	54.3	100	12	BM169322
682	11.4	54.3	83	29	EX287645	EX287645 ArabiDops	C 755	11.4	54.3	100	28	AZ803984
683	11.4	54.3	84	29	BZ592948	BZ592948 SALK_0514	C 756	11.4	54.3	100	28	BH905424
684	11.4	54.3	84	29	BZ592948	BZ592948 SALK_0514	C 757	11.4	54.3	100	28	BH905424
685	11.4	54.3	84	29	BZ592948	BZ592948 SALK_0514	C 758	11.4	54.3	100	28	BH905424
686	11.4	54.3	84	29	BZ592948	BZ592948 SALK_0514	C 759	11.4	54.3	100	28	BH905424
687	11.4	54.3	85	9	AA815657	AA815657 vt03f06.x	C 760	11.4	54.3	100	29	AL755565
688	11.4	54.3	85	12	BH082759	BH082759 ArabiDops	C 761	11.4	54.3	100	29	AL755565
689	11.4	54.3	85	28	BH411544	BH411544 L007023A0	C 762	11.4	54.3	100	29	AL755565
690	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 763	11.4	54.3	100	28	BH905424
691	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 764	11.4	54.3	100	28	BH905424
692	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 765	11.4	54.3	100	28	BH905424
693	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 766	11.4	54.3	100	28	BH905424
694	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 767	11.4	54.3	100	28	BH905424
695	11.4	54.3	87	9	AL906735	AL906735 ArabiDops	C 768	11.4	54.3	100	29	AL755565
696	11.4	54.3	87	9	AL906735	AL906735 ArabiDops	C 769	11.4	54.3	100	29	AL755565
697	11.4	54.3	87	13	BH212351	BH212351 604159708	C 770	11.4	54.3	100	29	AL755565
698	11.4	54.3	87	28	AZ511968	AZ511968 1M0357E14	C 771	11.4	54.3	100	29	AL755565
699	11.4	54.3	88	28	AZ511968	AZ511968 1M0357E14	C 772	11.4	54.3	100	29	AL755565
700	11.4	54.3	89	9	AV950400	AV950400 ArabiDops	C 773	11.4	54.3	100	29	AL755565
701	11.4	54.3	89	14	L47027	L47027 SCRRAP114.3	C 774	11.4	54.3	100	29	AL755565
702	11.4	54.3	89	28	BH866367	BH866367 SALK_1012	C 775	11.4	54.3	100	29	AL755565
703	11.4	54.3	90	28	AA909066	AA909066 om12e07.s	C 776	11.4	54.3	100	29	AL755565
704	11.4	54.3	90	28	BH408816	BH408816 L007000930	C 777	11.4	54.3	100	29	AL755565
705	11.4	54.3	90	29	BZ290897	BZ290897 SALK_0931	C 778	11.4	54.3	100	29	AL755565
706	11.4	54.3	90	29	BZ290897	BZ290897 SALK_0931	C 779	11.4	54.3	100	29	AL755565
707	11.4	54.3	91	28	AL767995	AL767995 ArabiDops	C 780	11.4	54.3	100	29	AL755565
708	11.4	54.3	91	28	AZ809624	AZ809624 2M0073010	C 781	11.4	54.3	100	29	AL755565
709	11.4	54.3	91	28	BZ290139	BZ290139 SALK_0235	C 782	11.4	54.3	100	29	AL755565
710	11.4	54.3	91	29	BZ597391	BZ597391 SALK_1035	C 783	11.4	54.3	100	29	AL755565
711	11.4	54.3	91	29	BX121368	BX121368 Dancio rer	C 784	11.4	54.3	100	29	AL755565
712	11.4	54.3	92	9	AI871069	AI871069 ArabiDops	C 785	11.4	54.3	100	29	AL755565
713	11.4	54.3	92	28	BH812709	BH812709 SALK_0623	C 786	11.4	54.3	100	29	AL755565
714	11.4	54.3	92	28	BH909707	BH909707 SALK_0555	C 787	11.4	54.3	100	29	AL755565
715	11.4	54.3	92	28	BZ292320	BZ292320 SALK_1238	C 788	11.4	54.3	100	29	AL755565
716	11.4	54.3	92	29	BZ292321	BZ292321 SALK_1238	C 789	11.4	54.3	100	29	AL755565
717	11.4	54.3	92	29	CC459173	CC459173 SALK_1256	C 790	11.4	54.3	100	29	AL755565
718	11.4	54.3	92	29	AL942757	AL942757 ArabiDops	C 791	11.4	54.3	100	29	AL755565
719	11.4	54.3	93	9	AI134517	AI134517 ArabiDops	C 792	11.4	54.3	100	29	AL755565
720	11.4	54.3	93	29	BZ292317	BZ292317 SALK_1238	C 793	11.4	54.3	100	29	AL755565
721	11.4	54.3	94	9	AA512503	AA512503 ArabiDops	C 794	11.4	54.3	100	29	AL755565
722	11.4	54.3	94	9	AA512503	AA512503 ArabiDops	C 795	11.4	54.3	100	29	AL755565
723	11.4	54.3	94	29	CC456041	CC456041 ArabiDops	C 796	11.4	54.3	100	29	AL755565
724	11.4	54.3	94	29	AL938406	AL938406 ArabiDops	C 797	11.4	54.3	100	29	AL755565
725	11.4	54.3	95	29	BZ593468	BZ593468 SALK_0738	C 798	11.4	54.3	100	29	AL755565
726	11.4	54.3	95	29	BZ593468	BZ593468 SALK_0738	C 799	11.4	54.3	100	29	AL755565
727	11.4	54.3	97	9	AA657348	AA657348 nt64a03.s	C 800	11.4	54.3	100	29	AL755565
728	11.4	54.3	97	9	AA657348	AA657348 nt64a03.s	C 801	11.4	54.3	100	29	AL755565
729	11.4	54.3	97	28	BH814682	BH814682 SALK_0668	C 802	11.4	54.3	100	29	AL755565
730	11.4	54.3	97	28	BH814682	BH814682 SALK_0668	C 803	11.4	54.3	100	29	AL755565
731	11.4	54.3	97	28	BH905413	BH905413 SALK_1067	C 804	11.4	54.3	100	29	AL755565
732	11.4	54.3	97	28	BZ564414	BZ564414 SALK_1289	C 805	11.4	54.3	100	29	AL755565
733	11.4	54.3	97	29	BZ593467	BZ593467 SALK_0738	C 806	11.4	54.3	100	29	AL755565
734	11.4	54.3	97	29	BZ597392	BZ597392 SALK_1035	C 807	11.4	54.3	100	29	AL755565

C 808	11.2	53.3	62	9	AA601097	AA601097 nos3g01..s	881	11.2	53.3	82	9	AA194434	AA194434 zq04f02..x
809	11.2	53.3	63	29	BZ287519	BZ287519 SALK 0208	882	11.2	53.3	82	12	BM493223	BM493223 EST00006
C 810	11.2	53.3	64	9	AI915515	AI915515 wg30a10..x	883	11.2	53.3	83	28	AZ791578	AZ791578 ZM0041K04
C 811	11.2	53.3	64	9	AV560973	AV560973 AV560973	884	11.2	53.3	84	9	AA684263	AA684263 vm68g12..s
C 812	11.2	53.3	64	10	BE228785	BE228785 SMOVL3CAN	885	11.2	53.3	84	28	BH810116	BH810116 SALK 0409
C 813	11.2	53.3	64	13	BQ739121	BQ739121 pt40f01..y	886	11.2	53.3	84	29	BZ663880	BZ663880 SALK 0274
C 814	11.2	53.3	66	9	AA458302	AA458302 sh86a08..y	887	11.2	53.3	85	9	AA060040	AA060040 m391e09..x
815	11.2	53.3	66	14	M00056	M00056 TGE8TY74D0	888	11.2	53.3	85	9	AA718968	AA718968 zh20h04..s
C 816	11.2	53.3	66	28	BH643834	BH643834 100806D01	889	11.2	53.3	85	9	AA951981	AA951981 AV951981
C 817	11.2	53.3	66	29	AL941813	AL941813 Arabidops	890	11.2	53.3	85	12	B1317990	B1317990 fg73c02..x
C 818	11.2	53.3	66	29	BK289557	BK289557 Arabidops	891	11.2	53.3	85	12	B1318004	B1318004 fg73e02..x
C 819	11.2	53.3	67	29	DME545229	DME545229 Drosophil	892	11.2	53.3	85	29	B2354887	B2354887 SALK 1259
C 820	11.2	53.3	67	13	BQ264657	AA269867 va55f10..x	893	11.2	53.3	86	9	AI559541	AI559541 t943h08..x
C 821	11.2	53.3	68	9	AU008270	AA264657 NISC 3704	894	11.2	53.3	86	13	B0865716	B0865716 S057E11 P
C 822	11.2	53.3	68	9	AU008297	AU008270 AU008270	895	11.2	53.3	87	9	AU012697	B38049 HS -1046-B2-
C 823	11.2	53.3	68	14	AM663254	AM663254 hh76c11..y	896	11.2	53.3	87	9	AU012700	AU007704 AU007704
C 824	11.2	53.3	68	18	CO1004	CO1004 HUMG8000397	897	11.2	53.3	87	28	BH186923	AU012697 AU012697
C 825	11.2	53.3	68	28	AZ309853	AZ309853 1M0017M08	898	11.2	53.3	87	28	BH609566	AU012700 AU012700
C 826	11.2	53.3	68	28	AZ340768	AZ340768 1M0072A14	899	11.2	53.3	87	28	BH857475	BH186923 032.P-09-
C 827	11.2	53.3	68	28	AZ815575	AZ815575 2M0083K20	900	11.2	53.3	87	28	BH857478	BH609566 HIV1B11
C 828	11.2	53.3	69	9	AM582804	AM582804 1BW Neutro	901	11.2	53.3	87	28	BH857478	BH857478 SALK 0725
C 829	11.2	53.3	69	13	BQ758141	BQ758141 Ehma01..SQ	902	11.2	53.3	87	29	B2352527	B2352527 SALK 0809
C 830	11.2	53.3	70	9	AI077347	AI077347 oy65g11..x	903	11.2	53.3	87	29	B2768249	B2768249 SALK 0809
C 831	11.2	53.3	70	29	BZ593095	BZ593095 SALK 0603	904	11.2	53.3	87	29	AL765961	AL765961 Arabidops
C 832	11.2	53.3	70	29	BZ595179	BZ595179 SALK 0862	905	11.2	53.3	87	29	CNS07RAJ	AL765961 Arabidops
C 833	11.2	53.3	71	28	BH847286	BH847286 SALK 0508	906	11.2	53.3	88	9	AA755755	AL765961 Arabidops
C 834	11.2	53.3	71	29	BZ595177	AA755029 vv75h08..x	907	11.2	53.3	88	9	AA415019	AA755755 t7 end of
C 835	11.2	53.3	72	9	AA755029	AA755029 vv75h08..x	908	11.2	53.3	88	13	BQ541094	AA755755 t7 end of
C 836	11.2	53.3	72	12	B1937436	B1937436 dd83e10..y	909	11.2	53.3	88	14	CH836236	AA415019 vc49h06..x
C 837	11.2	53.3	72	14	WB9090	WB9090 zh70h06..x1	910	11.2	53.3	88	14	AL77913	BQ541094 p86c0f07..y
C 838	11.2	53.3	73	10	BF727501	BF727501 SMOV3KCAM	911	11.2	53.3	88	14	AL77913	CB386236 OSTF041F7
C 839	11.2	53.3	73	10	BE058120	BE058120 sn11f04..y	912	11.2	53.3	88	29	AL77913	CB386236 OSTF041F7
C 840	11.2	53.3	73	10	BE058120	BE058120 sn11f04..y	913	11.2	53.3	89	13	BQ256730	AL77913 ym41d11..t1
C 841	11.2	53.3	73	10	BE058120	BE058120 sn11f04..y	914	11.2	53.3	89	13	BQ256730	AL77913 ym41d11..t1
C 842	11.2	53.3	73	10	BE058120	BE058120 sn11f04..y	915	11.2	53.3	90	13	B0862354	AL77913 ym41d11..t1
C 843	11.2	53.3	73	10	BE058120	BE058120 sn11f04..y	916	11.2	53.3	91	9	AA423416	AL77913 ym41d11..t1
C 844	11.2	53.3	74	28	AZ306924	AZ306924 1M0008N08	917	11.2	53.3	91	9	AA586853	AA423416 ve38h02..x
C 845	11.2	53.3	74	29	CC458994	CC458994 SALK 1234	918	11.2	53.3	91	28	AZ611942	AA586853 nm67f06..s
C 846	11.2	53.3	74	29	CC458994	CC458994 SALK 1234	919	11.2	53.3	91	28	BH244886	AZ611942 1M0438P01
C 847	11.2	53.3	75	12	BM259735	BM259735 sak19e09..y	920	11.2	53.3	91	28	BH244886	BH244886 MHA A02.
C 848	11.2	53.3	75	28	BH891943	BH891943 sak19e09..y	921	11.2	53.3	91	28	BH244886	BH244886 MHA A02.
C 849	11.2	53.3	75	29	AG250570	AG250570 Lotus Jap	922	11.2	53.3	92	9	AA517134	AA517134 sg45b09..y
C 850	11.2	53.3	75	29	CNS025H7	AA182068 Retradon	923	11.2	53.3	92	9	AA517134	AA517134 sg45b09..y
C 851	11.2	53.3	76	9	AA703311	AA703311 zj11a11..s	924	11.2	53.3	92	12	BM253592	AA517134 sg45b09..y
C 852	11.2	53.3	76	9	AI120991	AI120991 ub75f06..x	925	11.2	53.3	92	12	BM253592	AA517134 sg45b09..y
C 853	11.2	53.3	76	9	AI120991	AI120991 ub75f06..x	926	11.2	53.3	92	12	BM253592	AA517134 sg45b09..y
C 854	11.2	53.3	76	28	AZ566794	AZ566794 226PYE05	927	11.2	53.3	92	14	BM253592	AA517134 sg45b09..y
C 855	11.2	53.3	77	12	BF506925	BF506925 1116P-24b	928	11.2	53.3	93	12	BM253592	AA517134 sg45b09..y
C 856	11.2	53.3	77	12	BF506925	BF506925 1116P-24b	929	11.2	53.3	93	14	BM253592	AA517134 sg45b09..y
C 857	11.2	53.3	78	10	BF506925	BF506925 1116P-24b	930	11.2	53.3	93	14	BM253592	AA517134 sg45b09..y
C 858	11.2	53.3	78	12	BM253592	BM253592 EST00001	931	11.2	53.3	94	9	AI718525	AA517134 sg45b09..y
C 859	11.2	53.3	78	14	U77315	U77315 HSU77315 Hu	932	11.2	53.3	94	9	AI718525	AA517134 sg45b09..y
C 860	11.2	53.3	78	28	BH909096	BH909096 SALK 0519	933	11.2	53.3	94	9	AI718525	AA517134 sg45b09..y
C 861	11.2	53.3	78	29	AL937922	AL937922 Arabidops	934	11.2	53.3	94	10	BG156253	AA517134 sg45b09..y
C 862	11.2	53.3	79	9	AA128193	AA128193 z192a12..x	935	11.2	53.3	94	10	BG156253	AA517134 sg45b09..y
C 863	11.2	53.3	79	9	AU011979	AU011979 AU011979	936	11.2	53.3	94	10	BG156253	AA517134 sg45b09..y
C 864	11.2	53.3	79	10	BF506914	BF506914 1116P-24b	937	11.2	53.3	95	12	BM253592	AA517134 sg45b09..y
C 865	11.2	53.3	79	10	BF506914	BF506914 1116P-24b	938	11.2	53.3	95	12	BM253592	AA517134 sg45b09..y
C 866	11.2	53.3	79	12	BM285360	BM285360 EST00001	939	11.2	53.3	95	12	BM253592	AA517134 sg45b09..y
C 867	11.2	53.3	79	12	BM285360	BM285360 EST00001	940	11.2	53.3	96	28	AZ424093	AA517134 sg45b09..y
C 868	11.2	53.3	79	13	BO568258	BO568258 g1105a08..	941	11.2	53.3	96	28	AZ424093	AA517134 sg45b09..y
C 869	11.2	53.3	79	14	CA995251	CA995251 yg26d04..y	942	11.2	53.3	96	28	AZ424093	AA517134 sg45b09..y
C 870	11.2	53.3	79	28	BH789220	BH789220 SALK 0010	943	11.2	53.3	96	28	AZ424093	AA517134 sg45b09..y
C 871	11.2	53.3	79	28	BH789220	BH789220 SALK 0010	944	11.2	53.3	96	28	AZ424093	AA517134 sg45b09..y
C 872	11.2	53.3	80	9	AA908718	AA908718 o101d12..s	945	11.2	53.3	97	9	AA666842	AA517134 sg45b09..y
C 873	11.2	53.3	80	9	AL853232	AL853232 AL853232	946	11.2	53.3	97	9	AA666842	AA517134 sg45b09..y
C 874	11.2	53.3	80	28	BH808929	BH808929 100812A40	947	11.2	53.3	97	9	AA666842	AA517134 sg45b09..y
C 875	11.2	53.3	80	28	BH808929	BH808929 100812A40	948	11.2	53.3	97	9	AA666842	AA517134 sg45b09..y
C 876	11.2	53.3	80	29	AA837974	AA837974 Arabidops	949	11.2	53.3	97	9	AA666842	AA517134 sg45b09..y
C 877	11.2	53.3	81	9	AA837974	AA837974 Arabidops	950	11.2	53.3	97	12	BM253592	AA517134 sg45b09..y
C 878	11.2	53.3	81	9	AA837974	AA837974 Arabidops	951	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 879	11.2	53.3	81	9	AA837974	AA837974 Arabidops	952	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 880	11.2	53.3	81	9	AA837974	AA837974 Arabidops	953	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 881	11.2	53.3	81	9	AA837974	AA837974 Arabidops	954	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 882	11.2	53.3	81	9	AA837974	AA837974 Arabidops	955	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 883	11.2	53.3	81	9	AA837974	AA837974 Arabidops	956	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 884	11.2	53.3	81	9	AA837974	AA837974 Arabidops	957	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 885	11.2	53.3	81	9	AA837974	AA837974 Arabidops	958	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 886	11.2	53.3	81	9	AA837974	AA837974 Arabidops	959	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 887	11.2	53.3	81	9	AA837974	AA837974 Arabidops	960	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 888	11.2	53.3	81	9	AA837974	AA837974 Arabidops	961	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 889	11.2	53.3	81	9	AA837974	AA837974 Arabidops	962	11.2	53.3	97	28	AZ424093	AA517134 sg45b09..y
C 890	11.2	53.3	81	9	AA837974	AA837974 Arabidops	963	11.2	53.3	97	28	AZ424093	AA

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c 954 11.2 53.3 98 14 CA520780 KS11016H0
c 955 11.2 53.3 98 28 A2592186 A2592186 IM0402H24
c 956 11.2 53.3 98 29 B2663770 B2663770 SALK_0273
c 957 11.2 53.3 99 10 B2248200 B2248200 NF002G04D
c 958 11.2 53.3 99 11 CNS0813X BK012889 Single re
c 959 11.2 53.3 99 12 BM935438 BM935438 UI-M-BH3-
c 960 11.2 53.3 99 13 BQ287277 BQ287277 i165e03.x
c 961 11.2 53.3 99 29 AL757409 AL757409 Arabidops
c 962 11.2 53.3 100 9 AA015156 AA015156 m163a07.r
c 963 11.2 53.3 100 9 AA018711 AA018711 sd71906.y
c 964 11.2 53.3 100 9 AA459607 AA459607 sh89d02.y
c 965 11.2 53.3 100 9 AA582100 AA582100 MR3-ST019
c 966 11.2 53.3 100 9 AA781526 AA781526 sl81c04.y
c 967 11.2 53.3 100 9 AA513622 AA513622 nh29e11.s
c 968 11.2 53.3 100 10 BE151753 BE151753 QV3-HT030
c 969 11.2 53.3 100 12 BE762761 BE762761 QV3-NT002
c 970 11.2 53.3 100 12 BM447217 BM447217 DSA007D11
c 971 11.2 53.3 100 12 BM738230 BM738230 K-BEST0002
c 972 11.2 53.3 100 13 BM069148 BM069148 Arabidops
c 973 11.2 53.3 100 28 AF087410 AF087410 Arabidops
c 974 11.2 53.3 100 28 AF087410 AF087410 Arabidops
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c 976 11.2 53.3 100 29 CC044746 CC044746 3591_1.16
c 977 11.2 53.3 100 29 CC457081 CC457081 SALK_1061
c 978 11.2 53.3 100 29 BX002146 BX002146 Arabidops
c 979 11.2 53.3 100 29 A2581676 A2581676 Arabidops
c 980 11.2 53.3 100 29 TA256C04P TA256C04P T. brucei
c 981 11.2 53.3 100 29 TA83F04Q TA83F04Q T. brucei
c 982 11.2 53.3 100 28 A2759901 A2759901 1M0553H07
c 983 11.2 53.3 100 28 B2352519 B2352519 SALK_0809
c 984 11.2 53.3 100 29 B2352520 B2352520 SALK_0809
c 985 11.2 53.3 100 29 B2352521 B2352521 SALK_0809
c 986 11.2 53.3 100 29 B2352520 B2352520 SALK_0809
c 987 11.2 53.3 100 29 B2352521 B2352521 SALK_0809
c 988 11.2 53.3 100 29 B2352520 B2352520 SALK_0809
c 989 11.2 53.3 100 29 B2352521 B2352521 SALK_0809
c 990 11.2 53.3 100 29 B2352520 B2352520 SALK_0809
c 991 11.2 53.3 100 29 B2352521 B2352521 SALK_0809
c 992 11.2 53.3 100 29 B2352520 B2352520 SALK_0809
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c 994 11.2 53.3 100 29 B2352520 B2352520 SALK_0809
c 995 11.2 53.3 100 29 B2352521 B2352521 SALK_0809
c 996 11.2 53.3 100 29 B2352520 B2352520 SALK_0809
c 997 11.2 53.3 100 29 B2352521 B2352521 SALK_0809
c 998 11.2 53.3 100 29 B2352520 B2352520 SALK_0809
c 999 11.2 53.3 100 29 B2352521 B2352521 SALK_0809
c 1000 11.2 53.3 100 29 B2352520 B2352520 SALK_0809

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ALIGNMENTS

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RESULT 1
LOCUS AI218421 82 bp mRNA linear EST 30-NOV-1998
DEFINITION Q12410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1845595 3', mRNA sequence.
ACCESSION AI218421
VERSION AI218421.1 GI:3798236
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS 1 (bases 1 to 82)
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

```

Insert Length: 925 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 73.
 Location/Qualifiers
 1..82
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1845595"
 /lab_host="DH10B"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /note="Organ: pooled; Vector: PT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI CGAP CGBI) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 37 a 11 c 13 g 21 t
 ORIGIN

Query Match 77.1%; Score 16.2; DB 9; Length 82;
 Best Local Similarity 85.7%; Pred. No. 5.1e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTTCAGGAATTCANATC 21
 Db 46 AATTTCTAGGAATTAAGC 66

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RESULT 2
LOCUS CA339945 57 bp mRNA linear EST 04-NOV-2002
DEFINITION NISC_1y09d11.y1 NCI CGAP P132 Rattus norvegicus cDNA clone
IMAGE:5622956 5', mRNA sequence.
ACCESSION CA339945
VERSION CA339945.1 GI:24558043
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 57)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
info@image.llnl.gov
Plate: ILAM12449 row: G column: 21
Seq primer: M13P1 reverse primer (ABI).
Location/Qualifiers
1..57
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:5622956"
/sex="male"
/tissue_type="dorsal prostate"
/dev_stage="adult, 14 month"

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FEATURES

source


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/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP pr32"
/Note="Organ: prostate; Vector: pCMV-SPOK6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Constructed by Invitrogen. Note:
this is a NCI CGAP library."
BASE COUNT      15 a      15 c      12 g      15 t
ORIGIN
Query Match      72.4%; Score 15.2; DB 14; Length 57;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY
1 AGATTCTAGGATTCAAAT 20
29 ACATTCTAGGATTCAAAT 48
Db

RESULT 3
LOCUS      A2782789      84 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION 2M00023P07R Mouse 10kb plasmid UGCLM library Mus musculus genomic
A2782789
VERSION     A2782789.1 GI:12916863
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 84)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
JOURNAL
COMMENT     Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0023 row: P column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 84.
Location/Qualifiers
1..84
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCCM0023P07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCLM library"
/Note="Vector: pMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

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of pMD2 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      24 a      18 c      14 g      28 t
ORIGIN
Query Match      72.4%; Score 15.2; DB 26; Length 84;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY
1 AGATTCTAGGATTCAAAT 20
23 AGTTTCTAGTAATTCAGAT 42
Db

RESULT 4
LOCUS      CB405258      87 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION OSTR040A2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB405258
VERSION     CB405258.1 GI:30746985
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
ORGANISM    Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
1 (bases 1 to 87)
Reboul,D., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jena,S., Chevret,E., Papanicolaou,V., Toliaas,P.P.,
Placsek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.R. and Vidal,M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet. (2003) In press
JOURNAL
COMMENT     Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fcl.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact david_hill@fcl.harvard.edu or
marc_vidal@fcl.harvard.edu
POLYA=No.
Location/Qualifiers
1..87
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/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone lib="AD-wrmcDNA"
/Note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pC086"
BASE COUNT      24 a      19 c      19 g      25 t
ORIGIN
Query Match      72.4%; Score 15.2; DB 14; Length 87;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GATTTCAGGAATTCAAATC 21
 Db 41 GATTTCAGGAATTCAAATC 60

RESULT 5
 AL940051/c 91 bp DNA linear GSS 24-OCT-2002
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-243H10-014396,
 DEFINITION genomic survey sequence.

ACCESSION AL940051
 VERSION AL940051.1 GI:24396500
 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots;
 Spermatophyta; Magnoliopsida; Brassicales; Arabidopsis.
 rosids; eurosids II; Brassicaceae; Arabidopsis.

REFERENCE 1
 Strizhov N., Li Y., Rosso M., Viehoever P., Dekker K., Saedler H.
 and Weisshaar B.
 A pipeline for automated high-throughput generation of FSTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transposon lines

JOURNAL Unpublished
 REFERENCE 2
 Rosso M., Strizhov N., Li Y., Reiss B., Dekker K. and Weisshaar B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics

JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 91)
 Rosso M., Strizhov N., Li Y. and Weisshaar B.
 Direct Submission
 Submitted (21-OCT-2002) Weisshaar B. Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

REFERENCE 4
 TITLE This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone F1809. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 plant genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/
 Location/Qualifiers

FEATURES
 source 1..91
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone_lib="GK-243H10-014396"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA
 vector pAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT 35 a 19 c 9 g 28 t
 ORIGIN

Query Match 72.4%; Score 15.2; DB 29; Length 91;
 Best Local Similarity 85.0%; Pred. No. 1.5e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTTCAGGAATTCAAAT 20
 Db 67 AGTTTCAGGAATTCAGT 48

RESULT 6

BUS37156/c 93 bp mRNA linear EST 15-OCT-2002
 LOCUS T095D05 Populus apical shoot cDNA library Populus tremula x Populus
 tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION BUS37156
 VERSION BUS37156.1 GI:24019968
 KEYWORDS EST
 SOURCE Populus tremula x Populus tremuloides
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 93)
 Uneberg P., Bhalerao R.R., Jansson S. and Sterky F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries

JOURNAL Unpublished
 REFERENCE 2
 Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers

FEATURES
 source 1..93
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /tissue_type="apical shoot"
 /clone_lib="Populus apical shoot cDNA library"

BASE COUNT 32 a 13 c 16 g 32 t
 ORIGIN

Query Match 72.4%; Score 15.2; DB 13; Length 93;
 Best Local Similarity 85.0%; Pred. No. 1.5e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTTCAGGAATTCAAAT 20
 Db 58 AGATTTCAGGAATTCAAAT 39

RESULT 7
 BUS90262/c 97 bp mRNA linear EST 17-OCT-2002
 LOCUS P034B05 Populus petioles cDNA library Populus tremula cDNA 5 prime,
 DEFINITION mRNA sequence.

ACCESSION BUS90262
 VERSION BUS90262.1 GI:24101327
 KEYWORDS EST
 SOURCE Populus tremula
 ORGANISM Populus tremula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 97)
 Uneberg P., Bhalerao R.R., Jansson S. and Sterky F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries

JOURNAL Unpublished
 REFERENCE 2
 Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers

FEATURES
 source 1..97
 /organism="Populus tremula"
 /mol_type="mRNA"

/db xref="taxon:113636"
/tissue_type="petioles"
/clone_lib="Populus petioles cDNA library"
BASE COUNT 35 a 16 c 14 g 32 t
ORIGIN

Query Match 72.4%; Score 15.2; DB 13; Length 97;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTTCAGGAATCAAT 20
60 AGATTTCAGGAATCAAT 41

RESULT 8 AA749115 73 bp mRNA linear EST 27-JAN-1998
LOCUS ca58604.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309206 3',
DEFINITION mRNA sequence.
ACCESSION AA749115 GI:2789073
VERSION AA749115.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 73)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-rc@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtp/image/image.html
Insert Length: 805 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 65.

FEATURES
source location/Qualifiers

1..73
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1309206"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"

/note="Vector: pUT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTACCAATCGAAGTGGAGCGCGCCGTCATTTTCTTTT-3',
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pUT3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 29 a 10 c 7 g 27 t
TGIN

Y Match 69.5%; Score 14.6; DB 9; Length 73;
Local Similarity 81.0%; Pred. No. 2.7e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AGATTTCAGGAATCAATC 21
17 AGATTTCAGGAATTTAATC 37

RESULT 9 BZ593365

LOCUS BZ593365 93 bp DNA linear GSS 07-JAN-2003
DEFINITION SALX 070370.34.05.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALX_070370.34.05.n, genomic
survey sequence.

ACCESSION BZ593365 GI:27533884
VERSION BZ593365
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 93)

AUTHORS Alonso J.M., Leisee, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab,
C., Jeske, A., Karnes, M., Kim, C.U., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salik.edu

This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

FEATURES
source location/Qualifiers

1..93
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_070370.34.05.n"

/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"
BASE COUNT 31 a 12 c 16 g 34 t

Query Match 69.5%; Score 14.6; DB 29; Length 93;
Best Local Similarity 81.0%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTTCAGGAATCAATC 21
10 AGATTTCAGGAATCAATC 30

RESULT 10 AM695026 63 bp mRNA linear EST 21-DEC-2000
LOCUS AM695026/c NF082E06ST1F1050 Developing stem Medicago truncatula cDNA clone
AM695026
DEFINITION AM695026.2 GI:11957373
ACCESSION AM695026
VERSION AM695026
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)

```

ORGANISM      Medicago truncatula
               Burkariotia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
               ; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
               Medicago.
REFERENCE     1 (bases 1 to 63)
AUTHORS      He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
               ,C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,G.D. and Dixon
               ,R.A.
TITLE        Expressed Sequence Tags from the Samuel Roberts Noble Foundation
               Medicago truncatula stem library
JOURNAL      Unpublished
COMMENT      On Apr 14, 2000 this sequence version replaced gi:7569788.
               Contact: Dixon RA
               Plant Biology Division
               The Samuel Roberts Noble Foundation
               2510 Sam Noble Parkway, Ardmore, OK 73402, USA
               Tel: 580 221 7302
               Fax: 580 221 7380
               Email: radixon@noble.org
               Insert Length: 685 Std Error: 0.00
               Plate: 082 Row: E Column: 06
               Seq primer: TCACACAGGAACAGCTATGAC.
FEATURES
  source      Location/Qualifiers
               1..63
               /organism="Medicago truncatula"
               /mol_type="mRNA"
               /db_xref="taxon:3880"
               /clone="NF082E06ST"
               /tissue_type="stem"
               /dev_stage="Pooled developmental"
               /clone_1lb="Developing stem"
               /note="Vector: Lambda zap; Contains a mixture of
               internodal stem segments"
BASE COUNT   31 a 16 c 5 g 11 t
ORIGIN
Query Match 68.6%; Score 14.4; DB 9; Length 63;
Best Local Similarity 93.8%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY           5 TTCTAGGAATTCAAT 20
              ||| ||||| ||||| |||||
Db           30 TTGTAGGAATTCAAT 15

RESULT 11
CA513671/c 93 bp mRNA EST 15-NOV-2002
LOCUS      10-3_1H2 Porcine testis phage library Sus scrofa cDNA clone
DEFINITION 10-3_1H2, mRNA sequence.
ACCESSION  CA513671
VERSION     CA513671.1 GI:25014228
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 93)
AUTHORS   Burkin,H.R., Vieira,A.P. and Miller,D.J.
TITLE     Direct submission (Burkin, Vieira, Miller)
JOURNAL   Unpublished
COMMENT   Contact: Burkin HR
            University of Illinois at Urbana-Champaign
            1207 W Gregory Dr, Urbana, IL 61801, USA
            Tel: 217 244 5144
            Fax: 217 333 8286
            Email: burkin@uiuc.edu
            Insert Length: 93 Std Error: 0.00
            Plate: 10-3.1 Row: H Column: 2
            High quality sequence stop: 93.
            Location/Qualifiers
FEATURES
  source      1..93

```

```

BASE COUNT      23 a      24 c      17 g      29 t
ORIGIN
Query Match
Best Local Similarity 93.8%; Score 14.4; DB 14; Length 93;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 AGATTCCTAGCAATTC 16
        ||| ||||| ||||| |||
        16 AGACTCTTAGCAATTC 1

RESULT 12
LOCUS      AZ437380
DEFINITION 1M0225B12R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
            clone UGCG1M0225B12 R, genomic survey sequence.
ACCESSION  AZ437380
VERSION     AZ437380
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 97)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0225 row: B column: 12
            Seq primer: CACACAGCAACACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 97.
            Location/Qualifiers
                1..97
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UGCG1M0225B12"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_1b="Mouse 10kb plasmid UGCG1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The

```

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1/4732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 33 a 13 c 19 g 32 t

ORIGIN

Query Match 68.6%; Score 14.4; DB 28; Length 97;
Best Local Similarity 93.8%; Pred. No. 3.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTTCTAGGAATTCAAA 19
21 TTTCTAGGAATTCACA 36

RESULT 13
LOCUS BH851999
DEFINITION SALK_074019.36.90.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_074019.36.90.x, genomic survey sequence.

ACCESSION BH851999
VERSION BH851999.1 GI:21422870
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab,
AUTHORS 'C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shim,P.
Zimmerman,J. and Ecker,D.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL COMMENT
Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At5g16310 and 300 bases of the 5' end of At5g16320.
Class: TDNA tagged.

FEATURES
source location/Qualifiers

1..48
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_074019.36.90.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 12 a 4 c 12 g 20 t

ORIGIN

Query Match 67.6%; Score 14.2; DB 28; Length 48;
Local Similarity 84.2%; Pred. No. 3.8e-04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GATTTCAGGAATTCAAAT 20
28 GATTTCAGGAATTCAAAT 46

RESULT 14
LOCUS BG153679/c
DEFINITION BG153679 60 bp mRNA
nags8g08.x1 NCI_CGAP_Co26 Homo sapiens cDNA clone IMAGE:4225743 3', mRNA sequence.

ACCESSION BG153679
VERSION BG153679.1 GI:12665709
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 60)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL COMMENT
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LINL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: info@image.lnl.gov
Seq primer: -40UP from Gibco.

FEATURES
source location/Qualifiers

1..60
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4225743"
/tissue_type="normal colonic mucosa"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Co26"
/note="Organ: colon; Vector: PAMPI; mRNA made from normal colonic mucosa, cDNA made by oligo-dt priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA library preparation: David B. Krizman, Ph.D.
Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 17 a 17 c 9 g 17 t

ORIGIN

Query Match 67.6%; Score 14.2; DB 10; Length 60;
Best Local Similarity 84.2%; Pred. No. 3.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATTTCAGGAATTCAAAT 20
20 GAATTCAGGAATTCAGT 2

RESULT 15
LOCUS AI966296 83 bp mRNA
sc36h04.y1 Gm-cl014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl014-1232 5', mRNA sequence.

ACCESSION AI966296
VERSION AI966296.1 GI:5760933
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

1 (bases 1 to 83)
Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepcio, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35601 For further information call: (800)-533-4363 or contact via email: cduresgen.com
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 83
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl014-1232"
/tissue_type="leaves, 2-3 week old seedlings, greenhouse grown"
/lab_host="DH10B"
/note="Vector: pT73Pac (pT73, Pharmacia); Site 1: EcoRI; Site 2: HindIII. This cDNA library was constructed from mRNA isolated from leaves of 2-3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a 3' anchored poly (dT) primer. EcoRI adapters followed by ligated to the blunt-ended cDNA fragments restricted by digestion with EcoRI and HindIII. The cDNA fragments were directionally cloned into the EcoRI-HindIII restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelidg."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches

32 a 9 c 8 g 34 t

1 AGATTCTAGGATTCGAA 19
12 AAATTCAAGGATTCGAA 30

67.6%, Score 14.2; DB 9; Length 83;
84.2%; Pred. No. 4.1e+04;
0; Mismatches 3; Indels 0; Gaps 0;

RESULT 16
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

47 bp mRNA linear EST 11-DEC-2001
BU077154 NIBB Mochii normalized Xenopus tailbud library
laevis cDNA clone X1060a15 3', mRNA sequence.
BU077154
GI:17522070
EST.
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.
1 (bases 1 to 47)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.
Expressed genes in X. laevis embryo

JOURNAL
COMMENT
Unpublished
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 47
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="X1060a15"
/tissue_type="whole embryo"
/dev stage="stage 25"
/clone_id="NIBB Mochii normalized Xenopus tailbud library"

BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches

9 a 3 c 9 g 22 t 4 others

65.7%, Score 13.8; DB 12; Length 47;
88.2%; Pred. No. 5.7e+04;
0; Mismatches 2; Indels 0; Gaps 0;

3 ATTCTAGGATTCGAA 19
19 AGTTCTAGGATTCGAA 3

49 bp mRNA linear EST 16-OCT-1997
V14603.s1 Knowles Solter mouse unfertilized egg Mus musculus cDNA
clone IMAGE:835684 5', mRNA sequence.
AA422541
GI:2101361
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
Marra, M., Hillier, L., Allen, M., Bowers, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepcio, M., Tan, F., Underwood, K., Moore, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through INL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:495900
Seq primer: -40m13 fwd. RT from Amersham.
Location/Qualifiers
1. 49
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:835684"
/tissue_type="unfertilized egg"
/lab_host="DH10B"
/clone_id="Knowles Solter mouse unfertilized egg"
/note="Organ: unfertilized egg; Vector: pBluescribe (modified); Site 1: Mui; Site 2: SalI; Cloned

undirectionally from mRNA prepared from 5000 unfertilized eggs. Primer: Sall(dT):
 5'-CGGTGACGCGACCGTCTTTTCTTTT-3'. cDNAs were
 cloned into the MluI/SalI sites of a modified pBluescribe
 vector using commercial linkers (NEB). Average insert
 size: 1.0 kb."
 BASE COUNT 22 a 3 c 10 g 14 t
 ORIGIN

Query Match 65.7%; Score 13.8; DB 9; Length 49;
 Best Local Similarity 88.2%; Pred. No. 5.8e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAA 19
 1 |||||
 29 AGTCTAGGAATTCAAA 45

RESULT 18
 AZ810918/c

LOCUS 69 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0076K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0076K14 R, genomic survey sequence.
 AZ810918

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus

REFERENCE
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 69)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0076 row: K column: 14
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 69.
 Location/Qualifiers

FEATURES
 source

1. 69
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0076K14"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

BASE COUNT
 ORIGIN

Query Match 65.7%; Score 13.8; DB 28; Length 69;
 Best Local Similarity 88.2%; Pred. No. 6.1e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTCTAGGAATTCAAAT 20
 1 |||||
 27 TTCTAGGAATTCAAAT 11

RESULT 19
 AZ956832/c

LOCUS 69 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0223C05R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0223C05 R, genomic survey sequence.
 AZ956832

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus

REFERENCE
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 69)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0223 row: C column: 05
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 69.
 Location/Qualifiers

FEATURES
 source

1. 69
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0223C05"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 18 a 19 c 11 g 21 t

Query Match 65.7%; Score 13.8; DB 28; Length 69;
Best Local Similarity 88.2%; Pred. No. 6.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCGA 17
18 AGATTCTAGGAATTCGA 2

RESULT 20
BG153467/c 76 bp mRNA linear EST 05-FEB-2001
LOCUS nag99a01.x1 NCI_CGAP_CO29 Homo sapiens cDNA clone IMAGE:4204320 3',
DEFINITION mRNA sequence.
ACCESSION BG153467 GI:12665497
VERSION BG153467
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 76)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers

1..76
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4204320"
/tissue_type="tubulovillous adenoma"
/lab_host="DPH10B"
/clone_lib="NCI CGAP Co29"
/note="Organ: colon; Vector: PAMPI; mRNA made from colonic adenoma, CDNA made by oligo-dt priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. CDNA library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 22 a 20 c 14 g 20 t

Query Match 65.7%; Score 13.8; DB 10; Length 76;
Best Local Similarity 88.2%; Pred. No. 6.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATTCTAGGAATTCGA 18
24 GATTCTAGGAATTCGA 8

RESULT 21
BG151684 82 bp mRNA linear EST 05-FEB-2001
LOCUS nag63b11.x1 NCI_CGAP_CO26 Homo sapiens cDNA clone IMAGE:4226252 3',
DEFINITION mRNA sequence.
ACCESSION BG151684 GI:12663714
VERSION BG151684
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 82)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers
1..82
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4226252"
/tissue_type="normal colonic mucosa"
/lab_host="DPH10B"
/clone_lib="NCI CGAP Co26"
/note="Organ: colon; Vector: PAMPI; mRNA made from normal colonic mucosa, CDNA made by oligo-dt priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. CDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 22 a 21 c 14 g 24 t 1 others

Query Match 65.7%; Score 13.8; DB 10; Length 82;
Best Local Similarity 88.2%; Pred. No. 6.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATTCTAGGAATTCGA 18
40 GATTCTAGGAATTCGA 24

RESULT 22
BG151856 88 bp mRNA linear EST 05-FEB-2001
LOCUS nag65d05.x1 NCI_CGAP_CO26 Homo sapiens cDNA clone IMAGE:4226360 3',
DEFINITION mRNA sequence.
ACCESSION BG151856 GI:12663886
VERSION BG151856
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 88)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco.

FEATURES
 source
 Location/Qualifiers
 1..88

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4226360"
 /tissue_type="normal colonic mucosa"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Co26"
 /note="Organ: colon; Vector: pAMP1; mRNA made from normal
 colonic mucosa, cDNA made by oligo-dT priming.
 Directionally cloned into UDG sites. Size selected on
 agarose gel, average insert size 300 bp. Primary library.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 Reference: Krizman et al. (1996) Cancer Research
 56:5380-5383."

BASE COUNT
 ORIGIN
 23 a 23 c 17 g 25 t

Query Match
 Best Local Similarity 65.7%; Score 13.8; DB 10; Length 88;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
 Db
 2 GATTCTGAGAAATTCAA 18
 35 GAATTCGAGAAATTCAA 19

RESULT 23
 LOCUS
 EX533932
 DEFINITION
 Arabidopsis thaliana T-DNA flanking sequence GK-505B08-019718,
 genomic survey sequence.
 ACCESSION
 EX533932
 VERSION
 EX533932.1 GI:31411062
 KEYWORDS
 SOURCE
 ORGANISM

Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1

REFERENCE
 AUTHORS
 TITLE
 1 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.
 and Weishaar, B.
 A pipeline for automated high-throughput generation of ESTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 2 Unpublished

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 2 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 3 Strizhov, N., Li, Y., Rosso, M. and Weishaar, B.
 Direct Submission

COMMENT
 Submitted (02-JUN-2003) Weishaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion within the locus defined by clone F219. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 plant genomics program designated 'GABI'. Information on line
 availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.
 Location/Qualifiers

FEATURES

source

1..88
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-505B08-019718"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT
 ORIGIN
 30 a 12 c 16 g 30 t

Query Match
 Best Local Similarity 65.7%; Score 13.8; DB 29; Length 88;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
 Db
 2 GATTCTGAGAAATTCAA 18
 43 GATTCTGAGAAATTCAA 59

RESULT 24
 LOCUS
 CD028826/c
 DEFINITION
 mgmy001x18f.b Magnaporthe grisea MY Uni-Zap XR library Magnaporthe
 grisea cDNA clone mgmy001x18 5', mRNA sequence.
 ACCESSION
 CD028826
 VERSION
 CD028826.1 GI:30410282
 KEYWORDS
 SOURCE
 ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 1 (bases 1 to 91)
 Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatlerai
 K. and Dean, R.A.
 Expressed sequence tags from the rice blast fungus, Magnaporthe
 grisea

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 1 Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatlerai
 K. and Dean, R.A.
 Expressed sequence tags from the rice blast fungus, Magnaporthe
 grisea

Unpublished
 Contact: Ebbole DJ
 Department of Plant Pathology & Microbiology
 Texas A&M University
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
 Tel: 979 845 4831
 Fax: 979 845 6483
 Email: d-ebbole@tamu.edu
 Chromatogram file of this sequence is available, see contact person

PCR Primers
 FORWARD: T3 primer
 BACKWARD: T7 primer
 Plate: mgmy001 row: J column: 18
 Seq primer: T3

FEATURES
 source
 Location/Qualifiers
 1..91

/organism="Magnaporthe grisea"
 /mol_type="mRNA"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgmy001x18"
 /sex="Mat1-2 hermaphrodite"
 /cell_type="mycelium"
 /clone_lib="Magnaporthe grisea MY Uni-Zap XR library"
 /note="Vector: pBluescriptSK+; Site 1: EcoRI; Site 2: XhoI
 ; Unidirectional cloning. EcoRI site has T3 primer and
 predominantly 5' reads. T7 primer on XhoI side of insert."

Minimal medium mycelium library. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

BASE COUNT 43 a 13 c 19 g 16 t

Query Match 65.7%; Score 13.8; DB 14; Length 91;
Best Local Similarity 88.2%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAA 19
|||||
Db 37 ATTCTAGGAATTCATA 21

RESULT 25 AF087391 91 bp DNA linear GSS 18-APR-2000
LOCUS AF087391 Chlamydia trachomatis L2 Chlamydia trachomatis genomic
DEFINITION Clone 830 similar to RAD1 protein, genomic survey sequence.
ACCESSION AF087391 GI:7593958
VERSION AF087391.1
KEYWORDS GSS.
SOURCE Chlamydia trachomatis
ORGANISM Chlamydia trachomatis
REFERENCE Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
AUTHORS Wang, L., Steenbury, S.D., Zheng, Y. and Larsen, S.H.
TITLE Gene identification of Chlamydia trachomatis by random DNA sequencing
JOURNAL Unpublished
COMMENT Contact: Wang L.
Department of Microbiology & Immunology
Indiana University School of Medicine
635 Barnhill Drive, MS 255, Indianapolis, IN 46202, USA
Class: shotgun.

FEATURES

source location/Qualifiers
1. 91
/organism="Chlamydia trachomatis"
/mol_type="genomic DNA"
/strain="L2"
/db_xref="taxon:813"
/clone_1lb="Chlamydia trachomatis L2"
/note="isolate=4348"
BASE COUNT 33 a 18 c 11 g 29 t
ORIGIN

Query Match 65.7%; Score 13.8; DB 28; Length 91;
Best Local Similarity 88.2%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTC 17
|||||
Db 60 AGATTCTAGGAATTC 76

RESULT 26 BH758017 91 bp DNA linear GSS 01-MAR-2002
LOCUS BH758017 SALK 013098.27.85.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_013098.27.85.x, genomic survey sequence.
ACCESSION BH758017
VERSION BH758017.1 GI:19042773
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE

AUTHORS Alonso, J.M., Lelisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Kearns, M., Kim, C.T., Parker, H., Prednis, L., Shim, P., Zimmerman, J., and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At5g04410 and 300 bases of the 3' end of At5g04420.
Class: TDNA tagged.

FEATURES

source location/Qualifiers
1. 91
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_1lb="SALK 013098.27.85.x"
/note="TPCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html"
BASE COUNT 34 a 12 c 18 g 27 t
ORIGIN

Query Match 65.7%; Score 13.8; DB 28; Length 91;
Best Local Similarity 88.2%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAA 19
|||||
Db 51 ATTCTAGGAATTCATA 67

RESULT 27 BH615007 48 bp DNA linear GSS 28-JAN-2002
LOCUS BG00015-3prime Drosophila melanogaster P{GTL} P element insertion
DEFINITION lines Drosophila melanogaster genomic sequence recovered from 3' end of P element, genomic survey sequence.
ACCESSION BH615007
VERSION BH615007.1 GI:18379695
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE Lewis, R., Hoskins, R., Liao, G., Mozdén, N., Tsang, G., He, Y., Karpen, G., Bellen, H., Rubin, G. and Spradling, A.
TITLE The Berkeley Drosophila Genome Project Gene Disruption Project
JOURNAL Unpublished
COMMENT Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: getty@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P

element
The P element insertion position is base 1 in the 48 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
Class: transposon-tagged.

FEATURES
source Location/Qualifiers

1..48
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P[GT1] P element insertion lines"
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains one or more P[GT1] P-element transposon insertion. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <http://www.fruitfly.org/about/methods/inverse.pcr.html>."

BASE COUNT 17 a 5 c 10 g 16 t

Query Match 64.8%; Score 13.6; DB 28; Length 48;
Best Local Similarity 80.0%; Pred. No. 7.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAAATTCAAAT 20
|||||
6 AGATTGATCGGAATTTAAAT 25

Db

RESULT 28
LOCUS BF789276 50 bp mRNA linear EST 12-JAN-2001
DEFINITION 602105183P1 NCI CGAP Kid14 Mus musculus cDNA clone IMAGE:4223229
5', mRNA sequence.
ACCESSION BF789276
VERSION BF789276.1 GI:12094312
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLI at: <http://image.llnl.gov>
Plate: LHM9811 row: e column: 22
High quality sequence stop: 30.
Location/Qualifiers

1..50
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4223229"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI CGAP Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library. |"

FEATURES
source

BASE COUNT 19 a 7 c 9 g 15 t

ORIGIN

Query Match 64.8%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. No. 7.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAAATTCAAAT 20
|||||
15 AAATTCTAGGAAATTCAT 34

Db

RESULT 29
LOCUS BF463652/c 63 bp mRNA linear EST 04-DEC-2000
DEFINITION BF463652
UI-M-CG0p-bmp-a-11-0-UI.s1 NIH BMAP Ret4_S2 Mus musculus cDNA clone
UI-M-CG0p-bmp-a-11-0-UI 3', mRNA sequence.
ACCESSION BF463652
VERSION BF463652.1 GI:11532835
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 63)
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mes@mail.nih.gov

JOURNAL
MEDLINE
PubMed
COMMENT

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the retina tissue cDNA library Preparation: M.B. Soares lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 15-105, >B2#SINE/B2
Seq primer: M13 Forward
PolyA=yes.

FEATURES
source

Location/Qualifiers
1..63
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-bmp-a-11-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH BMAP Ret4_S2"
/note="Vector: pRTT-D-Pac (pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine
TAG_LIB=NIH_BMAP_Ret4_S2
TAG_TISSUE=adult-retina
TAG_SEQ=GTGAGCGCCGCC"

BASE COUNT 13 a 20 c 13 g 17 t

ORIGIN

Query Match 64.8%; Score 13.6; DB 10; Length 63;
 Best Local Similarity 80.0%; Pred. No. 7.4e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GATTCTAGAGATTCAAATC 21
 Db 38 GGTTGCTAGGATTCAGACTC 19

RESULT 30
 BG668331/c 71 bp mRNA linear EST 30-APR-2001
 LOCUS DRACOH10 Rat DRG library Rattus norvegicus cDNA clone DRACOH10 5',
 DEFINITION mRNA sequence.
 ACCESSION BG668331 GI:13890253
 VERSION BG668331
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus (Norway rat);
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 71)
 Xiao, H.S., Huang, Q.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C., Yang, L.,
 Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D., Zhang,
 X., Chen, Z., Han, Z.G. and Zhang, X.
 Identification of gene expression profile of dorsal root ganglion
 in the rat peripheral axotomy model of neuropathic pain
 Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
 22056133
 JOURNAL MEDLINE
 PUBMED 12060780
 COMMENT Contact: Zhang Xu
 Laboratory of Sensory System
 Institute of Neuroscience
 320 Yue Yang Road, Shanghai 200031, P.R. China
 Tel: 86-21-64748700-121
 Fax: 86-21-64713446
 Email: xu.zhang@ion.ac.cn
 This clone is also available at Chinese National Human Genome
 Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
 Pudong New Area, P.R. China. Please contact with Zhang Xu
 (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
 PCR Primers
 FORWARD: T3
 BACKWARD: T7
 Seq primer: T3
 POLYA=No.

FEATURES
 source Location/Qualifiers
 1..71
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="DRACOH10"
 /sex="male"
 /tissue_type="dorsal root ganglion"
 /dev_stage="adult"
 /clone_id="Rat DRG library"
 16 c 22 g 16 t

BASE COUNT 17 a 16 c 22 g 16 t
 ORIGIN

Query Match 64.8%; Score 13.6; DB 10; Length 71;
 Best Local Similarity 80.0%; Pred. No. 7.5e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGAGATTCAAAT 20
 Db 61 AGGTGCTGGAGATTCAGAT 42

RESULT 31
 BU890627

LOCUS BU890627 81 bp mRNA linear EST 17-OCT-2002
 DEFINITION P039E04 Populus petioles cDNA library Populus tremula cDNA 5 prime,
 mRNA sequence.
 ACCESSION BU890627
 VERSION BU890627.1 GI:24101692
 KEYWORDS EST.
 SOURCE Populus tremula
 ORGANISM Populus tremula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; Populus.
 1 (bases 1 to 81)
 Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 Unpublished
 JOURNAL Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
 source Location/Qualifiers
 1..81
 /organism="Populus tremula"
 /mol_type="mRNA"
 /db_xref="taxon:113636"
 /tissue_type="petioles"
 /clone_id="Populus petioles cDNA library"
 16 a 24 c 20 g 21 t

BASE COUNT 16 a 24 c 20 g 21 t
 ORIGIN

Query Match 64.8%; Score 13.6; DB 13; Length 81;
 Best Local Similarity 80.0%; Pred. No. 7.7e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGAGATTCAAAT 20
 Db 28 AGATCTAGCCACTCAAT 47

RESULT 32
 AA863156 86 bp mRNA linear EST 29-APR-1998
 LOCUS o991c09.s1 NCI CGAP Kids Home sapiens cDNA clone IMAGE:1455664 3'
 DEFINITION similar to gb:M12529 APOLIPOPROTEIN B PRECURSOR (HUMAN);, mRNA
 sequence.
 ACCESSION AA863156
 VERSION AA863156.1 GI:2955635
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 86)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: cgaps-rc@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILM at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 486 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham.
 Location/Qualifiers

FEATURES

```

source
1. .86
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1455664"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Kids"
/notes="Organ: kidney; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGAGAGATTGCGCGCGCATATTTTATTTTATTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT      13 a      28 c      21 g      24 t
ORIGIN
Query Match      64.8%; Score 13.6; DB 9; Length 86;
Best Local Similarity 80.0%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 2 GATTCTAGGAATTCATC 21
11 GATTGTAGGCTTCACTC 30

RESULT 33
BZ762984      87 bp      DNA      linear      GSS 13-MAR-2003
LOCUS      SALK_110771.31.45.x Arabidopsis thaliana T-DNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_110771.31.45.x, genomic
survey sequence.
ACCESSION      BZ762984
VERSION      BZ762984.1 GI:28935537
KEYWORDS      GSS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 87)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadinab
,C., Jeske,A., Karnes,M., Kim,C.U., Parker,H., Prednis,L., Shinn,P.
,Zimmerman,J. and Ecker,J.R.
A Sequence-indexed library of insertion Mutations in the
Arabidopsis Genome
Unpublished
JOURNAL
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
T-DNA.
Class: T-DNA tagged.
Location/Qualifiers
1. .87
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_110771.31.45.x"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more T-DNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can

```

```

BASE COUNT      35 a      17 c      10 g      25 t
ORIGIN
Query Match      64.8%; Score 13.6; DB 29; Length 87;
Best Local Similarity 80.0%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 AGATTCTAGGAATTCATC 20
68 AGCTTTTAGGTTTCAAT 49

RESULT 34
AL949242      90 bp      DNA      linear      GSS 24-OCT-2002
LOCUS      Arabidopsis thaliana T-DNA flanking sequence GK-319C03-015860,
genomic survey sequence.
DEFINITION      Arabidopsis thaliana T-DNA flanking sequence.
ACCESSION      AL949242
VERSION      AL949242.1 GI:24405864
KEYWORDS      GSS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 90)
Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone F9H3. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
http://www.mpiiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. .90
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-319C03-015860"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector PAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

BASE COUNT      32 a      11 c      15 g      30 t      2 others
ORIGIN
Query Match      64.8%; Score 13.6; DB 29; Length 90;
Best Local Similarity 80.0%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 AGATTCTAGCAATCAAT 20
 |||||
 DB 25 AGATGCTATCAATTTAAAT 6

RESULT 35
 LOCUS BU890255

DEFINITION BU890255 91 bp mRNA linear EST 17-OCT-2002
 P034A07 Populus petioles cDNA library Populus tremula cDNA 5 prime,
 mRNA sequence.

ACCESSION BU890255
 VERSION BU890255.1 GI:24101320

KEYWORDS EST.

SOURCE
 ORGANISM Populus tremula
 Populus tremula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eustosids I; Malpighiales; Salicaceae; Populus.

REFERENCE
 1 (bases 1 to 91)
 Umeberg, P., Balletero, R.R., Jansson, S. and Sterky, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 Unpublished
 Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
 source
 1..91
 /organism="Populus tremula"
 /mol_type="mRNA"
 /db_xref="taxon:113636"
 /tissue_type="petioles"
 /clone_lib="Populus petioles cDNA library"

BASE COUNT 18 a 25 c 22 g 26 t

ORIGIN

Query Match 64.8%; Score 13.6; DB 13; Length 91;
 Best Local Similarity 80.0%; Pred. No. 7.8e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGCAATCAAT 20
 |||||
 DB 40 AGATCTCTAGCCATCAAT 59

RESULT 36
 LOCUS D75616/c 92 bp mRNA linear EST 18-OCT-1999
 CE1K107D2F Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
 embryo Caenorhabditis elegans cDNA clone YK107d2 5', mRNA sequence.

ACCESSION D75616
 VERSION D75616.1 GI:1121403

KEYWORDS EST.

SOURCE
 ORGANISM Caenorhabditis elegans
 Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE
 1 (bases 1 to 92)
 Kohara, Y., Mitsui, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and
 Tabara, H.
 Toward an expression map of the C.elegans genome
 Unpublished
 Contact: Yuji Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855

TITLE
 JOURNAL
 COMMENT

FEATURES
 source
 1..92
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone_lib="YK107d2"
 /sex="hermaphrodite"
 /dev_stage="embryo"
 /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
 hermaphrodite embryo"

BASE COUNT 22 a 20 c 19 g 31 t

ORIGIN

Query Match 64.8%; Score 13.6; DB 14; Length 92;
 Best Local Similarity 80.0%; Pred. No. 7.8e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GATTCTAGCAATCAATC 21
 |||||
 DB 78 GAATTCAGCAATTTAATTC 59

RESULT 37
 LOCUS BH218165 94 bp DNA linear GSS 08-NOV-2001
 1006077E06.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
 survey sequence.

ACCESSION BH218165
 VERSION BH218165.1 GI:16810606

KEYWORDS GSS.

SOURCE
 ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
 1 (bases 1 to 94)
 Walbot, V.
 Maize genomic sequences found using engineered RescueMu transposon
 Unpublished
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1006077 row: 27
 Class: transposon-tagged.

FEATURES
 source
 1..94
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1006 - RescueMu Grid G"
 /note="Organ: leaf; Vector: RescueMu (engineered from
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'www.zmbd.iastate.edu' and follow the links for
 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
 extracted from leaf punches, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."

BASE COUNT 30 a 8 c 34 g 22 t

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished

COMMENT Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g27020.

FEATURES

source

Location/Qualifiers

1..100

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_119560.52.85.x"

/note="lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT

41 a 25 c 9 g 25 t

ORIGIN

Query Match

64.8%; Score 13.6; DB 29; Length 100;

Best Local Similarity 80.0%; Pred. No. 7.9e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

2 GATTCTAGAGAAATCAATC 21

DB

48 GATTTAGAGAGACTTGAATC 29

Search completed: February 4, 2004, 17:52:29
Job time : 1250.23 secs